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Minimum
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Gapop 10.0 , Gapext 1.0
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SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:
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ALIGNMENTS

RESULT AAH14327

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AAH14327 standard; cDNA; 2590

ВP

AAH14327;

26-JUN-2001

(first

entry)

Human cDNA sequence SEQ ID NO:11697.

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Ota T, I
Ishii S,
                                                       29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                          07-FEB-2001.
                                                                                                                                           EP1074617-A2
                                                                                                                                                                            Human; primer;
                                        (HELI-) HELIX RES INST.
                                                                                                          28-JUL-2000; 2000EP-0116126
                                                                                                                                                           Homo sapiens
              Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsı
                                                                                                                                                                            detection; diagnosis; antisense therapy; gene therapy;
               Wakamatsu
              Hayashi K, S
A, Nagai K,
               Saito K, Y
, Otsuki T;
                        Yamamoto
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comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC the So2 nucleotide sequences defined in the specification, where a primer set
CC the So2 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprises at polynucleotide which comprises of
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are useful for synthesising polynucleotides,
CC particularly without any specialised methods. AAH03166 to AAH13628 and
CC AAB9593 represent human amino acid sequences; and AAH13629 to AAH13620
CC CAB9593 represent invention.

CC of the present invention.
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                               BLUTSPENDEDIENST
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                                                                                  2000EP-0111696
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/note= "Binding site of p
complement (3034..3054)
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                                                                                                                                                                                                                                                                                                               'note=
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e 1 p34.1-p36; ds.
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CC RHD gene deletion in Rh negative haplotypes. The Rhesus genes

CC locus comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the

CC comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the

CC composed preferably the hybrid Rhesus box, the upstream Rhesus box

CC and/or the downstream Rhesus box. The RHD and RHCE genes are located at

CC composed 1 p34.1-p36. Rhesus box flanks the breakpoint region of the

CC RHD deletion in the common RHD negative haplotypes. The sequence has

CC been used to design primers which are useful for: (1) the specific

CC detection of the common RHD positive haplotypes in D-negative

CC individuals; (2) blood group typing; (3) determining whether a patient

CC can be transfused with RhD negative blood and whether blood is suitable

CC for transfusion to patients who should not be exposed to antigen C; (4)

CC assessing the risk of a RhD negative mother of conceiving or carrying an

CC RhD positive foetus. Anti-D antibodies are useful for treating pregnant

CC women who are Rhesus D negative, where the foetus is not homozygous for

CC the RHD gene to treat or prevent haemolytic disease of the newborn.
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Best Local S
Matches 844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 10; Fig 5; 135pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACTTTGAACTTCAGAGAGATGATTTAGAGTATCTGGCAGGAGAATTTCTAAGCAGCA 1318
AACCTTCGCCTAGATTAAAGAGGATGTGCCGGAAATGCCTGGATGCCCCAGTCAGAAGTTTG
                                                                aacctccaatcagaatttcagaagatatatggaaacccctggatgcccaggcagaagtttg
                                                                                                                                      CTGACGGGAGGCAAGGTAGAGCTTGGGGCTGTAGCTTCGGGGAGTGCAAGCCCCAAGCCTT
                                                                                                                                                                                                        CTCATGCTGTGCAGCCTAGGGACTTGGTGCCCTGCATCCCAGCCACTCCCAACCATGA
                                                                                                                                                                                                                          cctgtgctgtgtgcagcctagagacttggtgccctgtgtcccagtta------
                                                                                                                                                                                                                                                                            CTCCCATCACAGGTCCAGAGGTATCAGGAAAAAATGGTTTTGTTGGCCAGGCCCGGGGTC
                                                                                                                                                                                                                                                                                              atcaaatcactggcctggaggcct-aggagaaaatggttttgtgggacaggcccagggtc
                                                                                                                                                                                                                                                                                                                                                                aatcctcaagacaatggggaaaatatctcctggacatgtcagaggtcttcacagcagtcc
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                                                                                                                                                                                                                                                                                                                                              AATTCCCAAGACAATGGGGAAAATGTCTCCAGGGCATGTCAGAGGTCTTTATGGCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                844;
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                                                                                                                                                      46.5%;
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Pred. No. 2.4e-190;
0; Mismatches 178;
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31-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; RHCE; Rh negative; blood group typing; blood transfusion; antigen haemolytic disease of the newborn; chromosome 1 p34.1-p36; ds.
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2000EP-0111696
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The sequence represents the coding supstream Rhesus box of D positives.

sequence of . The Rhesus

of Rhesus genes

gene

Disclosure; Fig 9; 135pp; English.

nucleic acid molecular structure, positive haplotypes in D-negative

useful for detection of common individuals, comprises RHD, SM

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Local Similarity
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                                        gtccaccatcctccagactccagaagggtagatccactgacagcttgcagcatgtgcctg
                                                                                                                                                                                                     ctgtaggggtggggtcctcatggagaacctctgcaagggtagtacaaaagggaaatgttg
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79.1%;
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Pred. No. 4.5e-190;
0; Mismatches 178;
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The sequence represents the coding sequence of Rhesus gene locus:

downstream Rhesus box of D positives. The Rhesus genes locus
comprises the RHD, SMF1 and RHCE (all undefined) genes and/or the
comprises the RHD, SMF1 and RHCE (all undefined) genes and/or the
comprises the RHD, SMF1 and RHCE (all undefined) genes and/or the
comprises the RHD, SMF1 and RHCE (all undefined) genes are located at
comprises the RHD, SMF1 and RHCE genes are located at
chromosome 1 p34.1-p36. Rhesus box. The RHD and RHCE genes are located at
chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
RHD deletion in the common RHD negative haplotypes. The sequence has
been used to design primers which are useful for: (1) the specific
cheen used to design primers which are useful for: (1) the specific
detection of the common RHD positive haplotypes in D-negative
located the transfused with RhD negative blood and whether blood is suitable
for transfusion to patients who should not be exposed to antigen C; (4)
assessing the risk of a RhD negative mother of conceiving or carrying an
RHD positive foetus. Anti-D antibodies are useful for treating pregnant
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31-MAY-2000; 2000EP-0111696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; RHCE; Rh negative; blood group typing; blood transfusion; antigen haemolytic disease of the newborn; chromosome 1 p34.1-p36; ds.
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                                                                                                                                                                                                                                                                       Disclosure; Fig 10; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000; 2000WO-EP10745
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                                                                                                                                                                                                                                                                                                                         nucleic acid molecular positive haplotypes in
                                                                                                                                                                                                                                                                                                         RHCE genes
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D-negative
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                                                                                                                                                                                                                                                                                                                          useful for detection individuals, comprise
                                                                                                                                                                                                                                                                                                                         etection of common comprises RHD, SMP1
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Best Local Similarity
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                                                                                             aaaaatccacagacactcagtgccagcctgtgaaagcagcagggatggagtctgtaccct 1154
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gtccaccatcctccagactccagaagggtagatccactgacagcttgcagcatgtgcctg
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                                                     acaaaaccgtagtggcagagctgaccaagaccgtgggaatctacctcttgcattgtcatg
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                                                                                                                                                                                 ggtgggagcccccacagagtccccagtggggctccatctagtagagctgtgagaagaa
                                                                                                                                                                                                                                                      AACCTTCGCCTAGATTAAAGAGGATGTGCGGAAATGCCTGGATGCCCAGTCAGAAGTTTG
                                                                                                                                                                                                                                                                  aacctccaatcagatttcagaagatatatggaaacccctggatgcccaggcagaagtttg
                                                                                                                                                                                                                                                                                                                                                     CTCATGCTGTGCAGCCTAGGGACTTGGTGCCCTGCATCCCAGCCACTCCCAACCATGA
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Pred. No. 4.5e-190;
0; Mismatches 178;
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gaatatttggctaatgaggaagcaaatttttggctaataaggaagaaattttctaagcagca

Query Match
Best Local Similarity
Matches 844; Conserv

Conservative

46.5%;

Score 642.2; I Pred. No. 4.5e-0; Mismatches

.5e-190; les 178;

Indels Length

45;

Gaps 411

S

DB 22;

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RESULT 5
AAS03688/c
ID AAS03688;
XX AAS03688;
XX AAS03688;
XX PT 29-AUG-2001 (first XX PT 29-AUG-2001 (first XX PT 29-AUG-2001) (first XX PT 29-AUG-2001) (first XX PT 20-AUG-2000; RHD posi XW RHCE; Rh negative; by XX PT 200032702-A2.
XX Homo sapiens.
XX WO200132702-A2.
XX WO200132702-A2.
XX PD 10-MAY-2000; 2000W0-PT 31-OCT-2000; 2000W0-PT XX PT 31-MAY-2000; 2000W0-PT XX PT 2001-291052/30.
XX PT 1-2001-291052/30.
XX WPT; 2001-291052/30.
XX WPT; 2001-291052/30.
XX WPT; 2001-291052/30.
XX PT 2001-291052/30.
XX PT 31-MAY-2000; 2000W0-PT AHD POSITIVE haploty PT AHD Geletion in the Comprises to KRHD, SC Rhesus box (es), pref and/or the downstreact comprises the RHD, SC Rhesus box (es), pref and/or the downstreact comprises the RHD, SC Rhesus box (es), pref and/or the downstreact for the comprise foctus.
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CC RhD positive foctus.
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                                                                                                The sequence represents the coding sequence of Rhesus gene locus:

Chybrid Rhesus box of RHD negatives. The Rhesus genes locus

comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the

Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box

and/or the downstream Rhesus box. The RHD and RHCE genes are located at

chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the

RHD deletion in the common RHD negative haplotypes. The sequence has

been used to design primers which are useful for: (1) the specific

detection of the common RHD positive haplotypes in D-negative

individuals; (2) blood group typing; (3) determining whether a patient

can be transfused with RhD negative blood and whether blood is suitable

for transfusion to patients who should not be exposed to antigen C; (4)

assessing the risk of a RhD negative mother of conceiving or carrying an

RhD positive foetus. Anti-D antibodies are useful for treating pregnant

women who are Rhesus D negative, where the feetus is not homozygous for

the RHD gene to treat or prayers haemolytic disease of the newborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; RHCE; Rh negative; blood group typing; blood transfusion; antigen haemolytic disease of the newborn; chromosome 1 p34.1-p36; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecular RHD positive haplotypes in and RHCE genes -
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31-MAY-2000; 2000EP-0111696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccactggatttcggacttatatggggcccgtacccctttgtttttgccaatttttttccat 1334
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                                                                          to treat or prevent haemolytic disease of the
           2454 A; 2320 C; 2014 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135pp; English.
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D-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for detection of common individuals, comprises RHD, SM
              2453 T; 0 other;
                                                                                 newborn
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system disorder;

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aagcattcaagaggtgacttgggtgctgttaaaggcattcagtttcataagggaggcaga
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                                                             acctggacgtgagacatggagtcaaaagagatcattttggagctttaagatttgactgcc
                                                                                                                                                                                                                                                                    acaaaaccgtagtggcagagctgaccaagaccgtgggaatctacctcttgcattgtcatg
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24-FEB-2000
24-FEB-2000
16-MAR-2000
17-MAR-2000
17-MAR-2000
17-MAR-2000
17-MAR-2000
28-JUN-2000
29-JUN-2000
20-JUL-2000
11-JUL-2000
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; gene therapy; ds.
2000US-0227009
2000US-0229287
2000US-0229343
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2000US-0229344
2000US-0229345
2000US-0229509
2000US-0230438
2000US-0231443
2000US-0231244
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2000US-0231294
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2000US-0184664
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2000US-0188350
2000US-0198174
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RESULT AAL03635

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                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences commber of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence enceprotein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                 897
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         tgcccaggcagaagtttgctgtaggggtggggtcctcatggagaacctctgcaagggtag
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tgctcaggcaaaagtttgctccaggggcagagccttcatggagaacctctgctagggcag
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                                                                                                                                                                                                                                                                                 endocrine disorder; infection; wound heal
cell culture; chemotaxis; food additive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted
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216..353
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153..215
                                                                                                                                                                                                                                                                     identification;
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352 gaatatttggctaatgaggaagcaaattttggctaataaggaagaaatttctaagcagca 411

gaactttgatcttgagagagatgatttagggtatctggctgaagaaatttctaagcagca 1658

Query Match Best Local S Matches 835

Local 835;

Similarity

44.98; 78.38;

Score 620.4; Pred. No. 1.

DB 22;

Conservative

0;

Mismatches

1.7e-183; ches 192;

Indels Length

40;

Gaps

9

Sequence

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CC The secreted proteins and their genes are useful for preventing.

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Pathological conditions can be diagnosed by determining the

CC amount of the new protein in a sample or by determining the presence of

CC qualinclude developing products for the diagnosis or treatment of

CC and include developing products for the diagnosis or treatment of

CC and include developing products for the diagnosis or treatment of

CC and include developing products for the diagnosis or treatment of

CC allergies, neurological disorders, diseases of the immune system,

CC AIDS, autoimmune diseases (e.g., reumatoid arthritis), inflammation,

CC allergies, neurological disorders (e.g., Alzheimer's disease,

CC garkinson's disease), cognitive disorders, schizophrenia, asthma,

CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,

CC gastrointestinal disorders, pregnancy-related disorders, endocrine

CC disorders, and infections. The proteins can also be used to aid wound

CC sumburn, to maintain organs before transplantation, for supporting cell

CC culture of primary tissues, to regenerate tissues, to dentify their

CC cognate ligands or binding partners, and in chemotaxis, and can be used

CC antibodies specific for a protein of the invention can be used in

CC alleviating symptoms associated with the disorders mentioned above, and

CC indiagnostic immunoassays e.g., radioimmunoassay or enzyme linked

CC indiagnostic immunoassays e.g., radioimmunoassay or enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD05121-AAD05203 represent cDNAs corresponding to 24 human protein genes, and AAE01232-AAE01311 represent the proteins AAE01312-AAE01340 represent human secreted protein variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used
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30-JUN-2000; 2000US-0215130.
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                                                                                                                                                                      cctccaatcagatttcagaagatatatggaaacccctggatgcccaggcagaagtttgct
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The present invention describes an isolated peptide (I) consisting of an CC amino acid sequence selected from: (a) the amino acid sequence of a variant of the oestrogen receptor alpha (ESR-alpha) protein in AAG68251; CO r (b) a fragment comprising at least 10 contiguous amino acids of the protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and vascribe activities, and can be used in gene therapy and vaccine production. (I) is useful for identifying an agent that binds to (I), by contacting (I) with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to the peptide. A polynucleotide (II), encoding (I), is useful in the complex is formed with the agent bound to the genetiated/modulated by an oestrogen receptor (ER). (II) is also useful in gene therapy for treating cancer, osteoporosis and cardiovascular classases. The human ESR-alpha gene is located on chromosome 6. The present sequence represents the human ESR-alpha gene, which is given in
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20-OCT-2000;
24-JAN-2001;
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The present invention describes primer sets for synthesising your comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and comparticularly full-length cDNAs. The primers are also useful for the graticularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human amino acid sequences; AAB92446 to AAH13632 represent oligonucleotides, all of which are used in the exemplification.
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                                                                                                                                                                                                                                                    CC Sequences AAS44359-AAS44514 represent the SPINK5 gene, contigs and CC fragments of a SPINK5 clone, sequencing primers and PCR primers for SPINK5. SPINK5 encodes lympho-epithelial Kazal-type related inhibitor CC (LEKTI), a serine protease inhibitor. Susceptibility or predisposition to an atopic disease in a human subject can be detected by screening the genome for one or more polymorphic variants of SPINK5 gene and/or expression of a variant LEKTI protein in a tissue. Carrier status of a subject or development of Netherton's syndrome is diagnosed by screening for the presence of loss-of-function mutations in the SPINK5 gene. An expression vector compissing a nucleic acid encoding a serine protease inhibitor or its functional fragment can be used in screening for compounds with potential pharmacological activity by determining the serine protease activity of a protein previously identified as a ligand of the LEKTI protein. The atopic diseases include Netherton's Syndrome, as the status of a screen and hayfever.
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hayfever; antiasthmatic; antiallergic; antiinflammatory;
logical; PCR primer; sequencing primer; gene therapy.
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                                                                                                                                                                                                                                                                                                                                      Sequences AAS44359-AAS44514 represent the SPINK5 gene, contigs and configments of a SPINK5 clone, sequencing primers and PCR primers for SPINK5. SPINK5 encodes lympho-epithelial Kazal-type related inhibitor (LEKTI), a serine protease inhibitor. Susceptibility or predisposition to an atopic disease in a human subject can be detected by screening the genome for one or more polymorphic variants of SPINK5 gene and/or expression of a variant LEKTI protein in a tissue. Carrier status of a subject or development of Netherton's syndrome is diagnosed by screening for the presence of loss-of-function mutations in the SPINK5 gene. An expression vector comprising a nucleic acid encoding a serine protease inhibitor or its functional fragment can be used in screening for compounds with potential pharmacological activity by determining the serine protease activity of a protein previously identified as a ligand of the LEKTI protein. The atopic diseases include Netherton's Syndrome, as the account of the contract of the serior protein.
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining susceptibility to atopic disease or carrier status of Netherton's syndrome in humans by identifying variants of or mutations in SPINK5, a gene encoding lympho-epithelial Kazal-type related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; SPINK5; lympho-epithelial Kazal-type related inhibitor; L serine protease inhibitor; atopic disease; Netherton's syndrome; eczema; hayfever; antiasthmatic; antiallergic; antiinflammatory; dermatological; PCR primer; sequencing primer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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                                                                                                         aagcattcaagaggtgacttgggtgctgttaaaggcattcagtttcataagggaggcaga
                                              gcataagagttcagaaaatttgcaccctgacaatgtgataaaaaaaga--aaaacccattt
                                                                                                                                                       gaactttaaacttcagagagatgatttagggtatctggcagaagaaatttctaagcagca
tctgaggggaaattcaagctggctgcagaaatttgcatatgtaatgaggagctgaatgtt
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

anti-HIV;
antianaemic; a

antiarthritic;

Human excretory related polynucleotide

SEQ ID

NO 1019.

07-JAN-2002

(first

entry)

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antirheumatic; hepato antiparasitic; cardia antiparasitic; cardia antiparasitic; cardia antiparasitic; cardia antiparasitic; cardia aneurological disease; excretory system; ds. Homo sapiens. Homo sapi													
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cerebroprotective; antinflammatory; antilcer; anticonvulsant; antifungal; mune disorder; cardiovascular disorder; cardiovascular disorder; ion; nephrotropic; gene therapy; vaccine;													
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0179065.
2000US-0180628.
2000US-0184664.
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Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; viruoide; fungloide; opthalmological; antiallergic; hepatotropic; antidiabetic;
           gene therapy; cancer;
                           antiinflammatory; antiulcer;
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disease;
                                                                                                                         related
                                                                                                                                                      (first
                                                                                                                                                                                                                  DNA;
                                                                                                                                                     entry)
                                                                                                                        polynucleotide SEQ ID NO
infection;
              immune disorder;
                              vulnerary; anticonvulsant;
                                                                                                                                                                                                                  ₽P
              cardiovascular disorder;
                              antiparasitic;
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                                                       New isolated nucleic treating and/or preven
                             Disclosure;
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 invention relates
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2000US-0239937.
2000US-0241786.
2000US-0241786.
2000US-0241809.
2000US-0244817.
2000US-0244817.
2000US-0244817.
2000US-0244617.
2000US-0244647.
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2000US-0249217.
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2000US-02518856.
2000US-0251988.
2000US-0251989.
2000US-0251999.
                             SEQ ID NO
                                                                                                                                                            GENOME
                                                       preventing
                                                                                                                               sc,
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 ç
                             920;
novel kidney related polynucleotides
                                                        and polypeptides, useful for human diseases and disorders
                             564pp +
                                                                                                                               MS
                            Sequence Listing; English.
                                                              for diagnosing,
ders -
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בער הרבים הרבי הרבים הר

2000US-0186350.
2000US-018974.
2000US-0199874.
2000US-0199874.
2000US-0199875.
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2000US-0216880.
2000US-0216880.
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01-SEP-2000

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CC (AAI62971-AAI63793) and the encoded polypeptides (AAM42417-AAM42691)
CC collectively known as kidney antigens and the use of such kidney antigens
CC for detecting disorders of the kidney, especially kidney cancer and
CC kidney cancer metastases. The polynucleotides and proteins are also
CC e.g. by protein or gene therapy. The genes are isolated from a range
CC of human tissues disclosed in the specification. The nucleic acids,
CC proteins, antibodies and (ant)agonists are useful in the diagnosis,
CC treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,
CC and other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders
CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
CC sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC caractive infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.9%;
Best Local Similarity 79.1%;
Matches 813; Conservative
21452
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Note: The sequence da
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                                                                                                                 gatgcccaggcagaagtttgctgtaggggtgggggtcctcatggagaacctctgcaagggt 954
                                                                                                                                                                                                                 gtcaagaattgaggtttgggaacctccaatcagatttcagaagatatatggaaacccctg
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                         agtacaaaagggaaatgttgggtgggagcccccacacagagtcccccagtggggctccatc
                                                                                          GATGCCCAGGCAGAA-TTTGCTGCATGGGCAGGGCCCTTATGGAGAACCTCTACTAGGGC
                                                                                                                                                                                           GTCAAGAACTGGGGTTTGGGAACCTCCACCTAGATTTCAGAAGATGTATGGAAATGCCTG
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Pred. No. 3.9e-174;
0; Mismatches 161;
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16-MAR-2000

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18-APR-2000

19-MAY-2000

07-JUN-2000

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07-JUL-2000

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24-FEB-2000;
02-MAR-2000;
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cytostatic; gene therapy; vacci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2000;
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ine; metastasis; ds.
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33 - AUG - 2000; 31 - AUG - 2000; 01 - SEP - 2000; 01 - SEP - 2000; 01 - SEP - 2000; 05 - SEP - 2000; 05 - SEP - 2000; 06 - SEP - 2000; 06 - SEP - 2000;

5-0229343. 5-0229344. 5-0229345.

2000US-0226279

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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and ctreatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54950 and AAM82169 CC represent sevents used in the exemplification of the present invention.
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                                                                                                                                                                                              NUMBER OF SOURCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
ADDRESSEE: Thridge Avenue, Suite
                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        APPLICANT: Gregory Dolganov TITLE OF INVENTION: Human R
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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                                US-08-991-789A-29
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: Patent No. 6225054
: GENERAL INFORMATION:
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Best Local Similarity
Matches 387; Conserv
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 14855 base pairs
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                  1121 cctgtgaaagcaggagggatggagtctgtaccctacaaaaccgtagtggcagaggctgacc 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 01
FILING DATE: 26-JAN-1996
AFTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   1241 agagatcatttttggagctttaagatttgactgccccactggatttcggacttatatgggg 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                1061 ggtagatccactgacagcttgcagcatgtgcctgaaaaatccacagacactcagtgccag 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 14855 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sholtz, Charles REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                              cccgta-cccctttgttttggccaattttttccatttggaactgccgtatttacccaatg
                   cctgtacctccattgtatgta 1380
                                                                                                                                                                                                                                                                    aagaccgtgggaatctacctcttgcattgtcatgacctggacgtgagacatggagtcaaa 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catctagtagagctgtgagaagaagtccaccatcctccagact------ccagaag 1060
CCTGTATCCCCATTGTATCTA 14358
                                                                                                                                                                GGAGATCATTCTGGAGCTTTAAGATACACCTGCCCCACTGAATTTCGGACTTGCACGGGG
                                                                                                                                                                                                                                                 AAGGCCATGGAAGCCCACCTCTTGCATCAGAGTGACCTTGGATGTGAGACATGGAGTCAAA
                                                                                                                                                                                                                                                                                                                               CCTGTGAAAACAGCCAGGAAGGAGGCTATACCCTGCAAAGCC - - AGAAGTGGAGCTGCCC
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Pred. No. 9.7e-77
0; Mismatches 9
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APPLICANT: Frudakis, Tony N.

Smith, John M. Reed, Steven G

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; SEQUENCE DESCRIPTION: SEQ ID NO: 29: US-08-991-789A-29
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Best Local Simi
Matches 424;
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REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          1123
                                                                                                                                                                                                                                                                1065
                                                                 1181 aagaccgtgggaatctacctcttgcattgtcatgacctggacg-tgagacatggagtcaa 1239
1240 aagagatcattttggagctttaagatt---
                                                                                                                                                                                                                     302
                                                                                                                                 362
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APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                     --tgtgaaagcagggatggagtctgtaccctacaaaaccgtagtggcagagctgacc
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                            CATGAAAAAAAAACTGAGAAGAAGACTGTNCCCTACAATGCCACCGGAGCAGAACTGCCC
                                                                                                                                                                                                                                                                                                       GAACACTGCCTAATGAAACTGTGAGAAGATGGCCACTGTCATCCAGACACCAGAATGATA
                                                                                                                                                                                                                                                                                                                             CTAACACCTAGATATTCAGACAAAAGTTTACTACAGGGATGAAGCTTTCACGGAAAACCT
                                                                                                                                                                                                                GACCCACCAAAAACTTATGCCATATTGCCTATAAAACCTACAGACACTCAATGCCAGCCC 361
                                                                                                                                                                                                                                       gatccactgacagcttgcagcat-gtgcctgaaaaatccacagacactcagtgccagcc- 1122
                                                                                                                                                                                                                                                                                                                                                                                           CTACTAGGAAAGTACAGAAGAGAAATGTGGGTTTGGAGCCCCCAAACAGAATCCCCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGCCATGGAAGCACAGCTCTTATATCAATGTGACCTGGATGTTGAGACATGGAATCCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGGGTACCAGCCCCAAGCCTTGACAACTTCCATAGGGTGTCAAGCCTGTGGGTGCACA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMpatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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-tgactgcccactggatttcggacttata 1295
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                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                              Matches 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE_POCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1296
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Smith, John M. APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                945
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                                                                                                                                                                                                              772 agagggtgcaagccccaagccttggcagcttccaagtggtgttgagcctgtgggtgcaaa 831
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                                                   122 CTAACACCTAGATATTCAGACAAAAGTTTACTACAGGGATGAAGCTTTCACGGAAAACCT 181
                                                                   887 --aacccctggatgcccaggcagaagtttgctgtaggggtgggggtcctcatggagaacct 944
                                                                                                                                                       832
                                                                                                                        62
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                            N
ctgcaagggtagtacaaaagggaaatgttgggtgggagcccccacacagagtcccccagtg 1004
                                                                                                                     caatgcctgtacctccat 1372
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                                                                                                                                                                                            AGAGGGTACCAGCCCCAAGCCTTGACAACTTCCATAGGGTGTCAAGCCTGTGGGTGCACA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATGCCTGTNCCCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                      linear
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04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                                              Score 247.4; DB 4;
Pred. No. 1.7e-69;
                                                                                                                                                                                                                                                            ed. No. 1.7e-69;
Mismatches 177;
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                                                                                                                                                                                                                                                                                               Length
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CURRENT FILING DATE: 1988-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09128155 Patent No. 6117654
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 572; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 16
                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C
-09-128-155-16
                                                                                                                71252
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                 71312
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 152331
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nilarity 59.48;
Conservative
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Pred. No. 1e-65;
0; Mismatches 320;
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RESULT 6
US-08-687-080-59
; Sequence 59, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
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APPLICANT: Gregory Dolganov TITLE OF INVENTION: Human RUNGBER OF SEQUENCES: 175
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CORRESPONDENCE ADDRESS:

ADDRESSEE:
STREET: 3
CITY: Pal
STATE: CA

Palo Alto : CA

350 Cambridge

Dehlinger & Associates

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US-08-687-080-59
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Best Local Similarity
Matches 340; Conserv
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INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 14855 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324 0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/592,126 FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5174 GAGATCTGAAACTGGAACTTATATTTAAAAAGGGAAGCAGAGCATAAAAGTTTTGGAAAATT 5233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
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tttgctgtaggggtgg 926
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                                                                                                                                                     ccttggcagcttccaagtggtgttgagcctgtgggtgcaaagaagtcaagaattgaggtt 850
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                                                                                                                                                                                                                                                                                                          cctaggagaaaatggttttgtgggacaggcccagggtccctgtgctgtgtgcagcctaga 730
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                                                          TGGGAGCCTCCACCTAGATTTCAGGGGATGTATGGAAACGTCTGGATGTCCAGGCAGAAG
                                                                           tgggaacctccaatcagatttcagaagatatatggaaacccctggatgcccaggcagaag 910
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Pred. No. 1e-54;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                    Query Match 3.5%; Score 48.8; DB 1; Best Local Similarity 4.9%; Pred. No. 4.3e-05; Matches 17; Conservative 192; Mismatches 139
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                     1282
                                                                                                                                                                    1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                     aaattcaagctggctgcagaaatttgcatatgtaatgaggagctgaatgttaatcctcaa 598
                                                                                           agttcagaaaatttgcaccctgacaatgtgataaaaaagaaaaacccattttctgagggg 538
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5670367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7218 base pairs
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(703)683-4109
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; LOCATION:
US-08-463-911-6
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US-08-463-911-6
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Best Local :
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                                                                                                                                                                                                                                                                  Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 111
MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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222 agcccatcatcttcacaggggtcctgtacaatgcccagagggatttaaaggaggccatgg 281
                                                       398
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                                                                                                                                                     102 gtgcaccaggtttaccacaatatacaggagaaataagtgaaatgacaaaatgcccctgtc 161
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                                                                                                                                                                                                                    42 atgtagaagttgctggacctccagcacaccccaggcccccagaagaagtggggcctcctg 101
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OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/463,911
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                                                                      ctgatatagaaaggtcagcctttactgtgaagctcagtggaaaacttcctcttcctttca 221
                                                                                                                       GTCCCCGAGGCTTTCCGGGAATCCAAGGCAGGAAAGGAGAACCTGGAGAAGGTGCCT--- 397
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                                                                                                                                                                                                                                                                                Similarity
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Two Militia Drive
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                            3.5%;
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A NOVEL SERUM PROTEIN PRODUCED EXCLUSIVELY IN ADIPOCYTES
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                                                                                                                                                                                                                                                              Score 48.4; DB 2;
Pred. No. 2.1e-05;
0; Mismatches 166;
                                                                                                                                                                                                                                                                                              Length 1313;
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US-09-188-930-217
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                                              Sequence 217, Application US/09188930A Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
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; ORGANISM: Homo sapiens
US-09-140-804-9
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US-09-140-804-9
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09140804 Patent No. 6197930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
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CURRENT FILING DATE: 1998-08-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4517
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529 tgaaggatgtgaaggtcagcctcttcaagaaggaca 564
                       342 attgcaaggtgaatatttggctaatgaggaagcaaa 377
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Pred. No. 4.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                166;
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APPLICANT: Onrust, Rene APPLICANT: Murison, James Greg TITLE OF INVENTION: Compositions Isolated From

Skin Cells

Sleeman, Matthew

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; ORGANISM: Rat
US-09-188-930-217
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Best Local S
Matches 103
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CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                              TELEFAX: (617) 861-954
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                             NAME: Granahan, Patricia
REGISTRACION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1107
                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Scherer, Philip
APPLICANT: Lodish, Harvey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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mes 103; Conserv
                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
              STRANDEDNESS:
                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Lexington
                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
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Two Militia Drive
                                              1276 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                USA
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linear
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            single
                                                                                               861-9540
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Harvey F.
A NOVEL SERUM PROTEIN PRODUCED EXCLUSIVELY IN ADIPOCYTES
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                                                                                                                                                                                                                                                       US/08/463,911
                                                                                                                                                     WHI95-05
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US-08-543-246B-8
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Best Local S
Matches 106
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                               TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                    FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff "-"
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 28-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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TYPE: n
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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LOCATION:
                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 07901-1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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ADDRESSEE: NO 6262244artis Corporation
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06; Conservative
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                1755 base pairs
                                                                      908-522-6955
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Pred. No.
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; LOCATION: (198)...(926)
US-09-140-804-1
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US-09-140-804-1
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
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NAME/KEY:
LOCATION:
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                                                                                                                               326 gatgttgagctgcatcattgcaaggtgaatatttggctaatgaggaa 372
                                                                                                     663 catgccaccgtctaccgggccagcctgcagtttgatctggtgaagaa 709
                                                                                                                                                                                 266 ttaaaggaggccatgggagtctttgcttgcagggtgcctgggaattactactccagcttt 325
                                                                                                                                                                                                                         543 cctccgccgtctgacgcacccttgcccttcgaccgcgtgctggtgaacgagcagggacat 602
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LOCATION:
                                                                                                                                                              tacgacgccgtcaccggcaagttcacctgccaggtgcctggggtctactacttcgccgtc 662
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Pred. No. 0.
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; OTHER INFORMATION: Degenerate nucleotide sequence ; OTHER INFORMATION: polypeptide of SEQ ID NO:2. US-09-140-804-10
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Appli
Patent No. 5866341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/140,804 CURRENT FILING DATE: 1998-08-26
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                APPLICANT: SPINELLA, Dominic
APPLICANT: BECHERER, Kathleen
APPLICANT: BROWN, Steven
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: SCREENING DRUG LIBRARIES
NUMBER OF SEQUENCES: 19
                                                    ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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              COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                 COUNTRY:
                                                                                                                                   STATE:
                                                                                                                                                   CITY: San Diego
                                                                                                                                                                     ADDRESSEE: Gen-Probe Incorporated STREET: 10210 Genetic Center Drive
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27.9%; Pred. No. 0.12;
tive 33; Mismatches 189;
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INFORMATION FOR SEQ ID NO: 15.
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 1inear
US-08-627-151A-15
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Search completed: June 30, 2002, 14:37:29 Job time: 6695 sec
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Best Local Similarity 54.1%;
Matches 73; Conservative (
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APPLICATION NUMBER: US/08/627,151A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CBIO16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-410-8926
TELEFAX: 619-410-8928
                                                                              888 GGAGTTCGGGCAAGG 902
                                                                                                   828 CTGTGTCATCCACGACGCCTGGAGCGGCCTGAGGCACGTGGTGCAGCTTCGTGCCCAGGA 887
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June 30, 2002, 11:48:13; Search time 1615.67 Seconds (without alignments) 11536.573 Million cell u
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BM457166 AGENCOURT
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BM472108 AGENCOURT
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VERSION
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AUTHORS
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                                                               Query Match 49.1
Best Local Similarity 80.5
Matches 859; Conservative
                                                                                                                                                                                                                                            source
Email: luxingwwe263.net
full-length and coding sequence.
Location/Qualifiers
1. 2615
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="human bone marrow cDNA library"
/tissue_type="bone marrow"
705 a 531 c 641 g 738 t
                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: xingwu Lu,liangxian Cui,yonghai Li
Department of Biochemistry
Institute of Basic Medical Science, Peking Union Medical College
DongDan SanTiao 5, Beijing, P.R.C, 100005
Tel: 86-010-65296951
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BE420422
BE420422.1 GI:16041640
EST.
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                                                              Score 677.8; DB 10;
Pred. No. 1.9e-182;
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Eukaryota; |
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Submitted (12-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov
Series: IRAL Plate: 14 Row: d Column: 7
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephan
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Rubin La
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BC004496.1 GI:14709139
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immalia; Eutheria;
(bases 1 to 2009)
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/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
429 c 513 g 511 t
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/db_xref="taxon:9606"
/clone="IMAGE:3831313"
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                   44.6%;
78.1%;
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Primates;
Score 615.8; DB 11;
Pred. No. 9.6e-165;
D; Mismatches 207;
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                                    Lu,X., Cui,L. and Li,Y.

DDRT-PCR from B cell
Unpublished (2000)
Contact: xingwu Lu,liangxian Cui,yonghai Li
Department of Biochemistry
Institute of Basic Medical Science, Peking
DongDan SanTiao 5, Beijing, P.R.C, 100005
Tel: 86-010-65296951
Email: luxingwu@263.net
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1 (bases 1 to 1036)
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Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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BM471183
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AGENCOURT_6478314 NIH_MGC_72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                      -gctgtggcttcagagggtgcaagccccaagccttggcag---cttccaagtggtg
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5563049"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
Technologies."
a 239 c 294 g 247 t 2 others
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77.7%;
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Pred. No. 7.4e-127;
0; Mismatches 151;
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ACCESSION
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TITLE
JOURNAL
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603021014F1 NIH_MGC_114
                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11479 row: k column: 04
                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 870)
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EST.
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BI488505
                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                       quality sequence stop: 849.
             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5191803"
/clone_lib="NIH_MGC_114"
                                                                                                    Location/Qualifiers
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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BASE COUNT
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Best Local Sim
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              aaagagatcattttggagctttaa-gatttgactgccccactggatttcggacttatatg
                                                                                        CCBAGACCGTGGGAACCTACCTCTTGCATTGTCATGACCTGGACGTGAGACATGGAGTCA 1238
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ATGGTAGATCCACCAACAGCTTGCACCATGTGCCTGGAAAAGATGCAGGTACTCAATGCC
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                                                                    CCAAGACCATGGGAACCCACTCTTGCATCAGCGTGACCTTGGATGCGAGACCTGGAGTCA
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76.1%;
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Pred. No. 8.
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3.5e-126;
hes 168;
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5', mRNA sequence.
BM457166
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Tissue Procurement: ATCC
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Contact: Robert Strausberg,
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/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xref="taxon:9606"
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                                                                                    GCCGCAGACATTCAACACCAGCCCGGGGAAGCAGCCAAAAGGGGGGGAATATATCCTGCCA
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/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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Pred. No. 5.1e-121;
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ccacacagagtccccagtggggctccatctagtagagctgtgagaagaagtccaccatcc
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                                                  GTCCGCGGAGCTCAGGCTGTGGCTTCAGAGGGTGCAAGCCCTAAGCCTTGGCAGCTTCCA
                                                                                                                   506;
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama, A., Hattori, M., Toyoda, A.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-085H08.F.
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Pan troglodytes DNA,
AG086951
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee Male
189 c 195 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-085H08.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
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82.4%;
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Pred. No. 7.2e-112;
D; Mismatches 106;
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nd Sakaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG064424
Pan troglodytes DNA, clone: PTB-053H2
AG064424
AG064424.1 GI:16616226
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone: PTB-053H24.R.
                                                                                                                                                                                                                                                                                      clone tracking
                                                                                                                                                                                                                                                                                                       Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                           (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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                /cell_type="lymphoblast"
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AG112666
AG112666.1 GI:16733185
GSS; GSS (genome survey s
Pan troglodytes male lymp
BAC Library clone:PTB-119
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama,
Submitted (RIKEN), Genomic
                                                                                                                                           Pan troglodytes
Eukaryota; Metazoa; Chordata;
""mmalia: Eutheria; Primates;
                                                                                               Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                              Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                          Taylor, T.D.,
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                                                   CCTGTAGCCCCTTAGTTATGGCCAATCTCTCCCATTTGGAATGGCTGCACTTCACCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC ences generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanze
/174 c 180 g 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-119B01.R"
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Pred. No. 1.9e-106;
0; Mismatches 106;
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                tatggaaacccctggatgcccaggcagaagtttgctgtaggggtgggggtcctcatggaga
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                                                                                                                                                         GCGGGTGCACAGAAGTCAAGAATTGAGGTGTGGGAACCTCTAACTAGATTTCAGAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCMS12 row: e column: 07 High quality sequence stop: 714.
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1 (bases 1 to 721)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT prining. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
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Pred. No. 2.6e-106;
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                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10611 row: 1 column: 19
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                          quality sequence stop:
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; vector: pCMV-SPORR6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo of Average insert size 1.5kb. Library constructed by Lil Technologies. Note: this is a NCI_CGAP Library."

1 216 c 273 g 196 t
                                                                                                                                      /clone="IMAGE:4752858"
/clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                               organism="Homo sapiens"
/db_xref="taxon:9606"
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by Life
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Local Similarity 10...
645; Conservative
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                                                                                                   mRNA sequence.
BG281182
BG281182.1 GI
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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602402107F1 NIH_MGC_20
                                                                                                      GI:13030107
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76.9%;
Chordata;
Primates;
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Craniata; Vertebrata;
Catarrhini; Hominidae
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  Hominidae;
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IMAGE:4544448 5',
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Best Local Similarity 77.5
Matches 571; Conservative
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                   acccctggatgcccaggcagaagtttgctgtaggggtggggtcctcatggagaacctctg
                                                                                                   caaagaagtcaagaattgaggtttgggaacctccaatcagatttcagaagatatatggaa
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                                                                                CACAGAAGTCAAGAATTGAGGTTTGGGAACCTCCACCTAGATTTCAGAGGA-GTATGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9666"
/clone="nMAGE:4544448"
/clone=lib="NILHMGC_20"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host="bH10B (phage-resistant)"
/
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77.5%;
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Pred. No. le-104;
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                    655 atcactggcctggaggcctaggag---aaaatggttttgtgggacaggcccagggtccct 711
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ATCACAGACCCAGAAGCCTAGGAGCAAAAAAATGCTTTTGTGGTCTGGACCCAAGGTCCCC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctccatctagtagagctgtgagaagaagtccaccatcctccagaactccagaagggtagat 1067
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BI754555
BI754555.1 GI
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11485 row: g column: 21
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National Institutes of Health, Mammalian
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 736)
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603023384F1 NIH_MGC_114 Homo
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                                                                                                                                                                                 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 733.
Location/Qualifiers
                                                                                                                                                                      /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5194028"
/clone=lib="NIH_MGC_114"
                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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                                                                     Score 404.6; DB 10;
Pred. No. 1.8e-104;
D; Mismatches 134;
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap.
                                                   Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                        Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                 AG062447.1 GI:16614249
GSS; GSS (genome survey sequence).
RSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-050M20.F.
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                                                         gagacatggagtcaaaagagatcattttggagctttaagattttgactgccccactggatt 1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
This BAC end clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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/db_xref="taxon:9598"
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/sex="male"
/sex="male"
/cell_type="lymphoblast"
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REFERENCE AUTHORS RESULT HS302D9 COMMENT SOURCE ORGANISM ACCESSION KEYWORDS VERSION DEFINITION Locus JOURNAL TITLE Direct Submission
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 13, 1999 this sequence version replaced gi:3164067.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145880) HS302D9 145880 bp DNA linear PRI 12-DEC-19
Human DNA sequence from clone RP1-302D9 on chromosome 22 Contains Bridgeman,A. Homo sapiens Z82198.2 GI:6572207 variation annotation may not be found complete sequence. חב the sequence submission PRI 12-DEC-1999

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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. All). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence
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VECTOR: pCYPAC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s sequence is the entire insert of of clone CTA-282F2 is at 69682 in of clone CTA-415G2 is at 55167 in
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                                                                                                                                                                                                                                                                                             /note="MLTIE repeat: 3929. .4278
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1033. .1336
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4279. .4485
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/note="AluSc repeat: matches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                              073. .5176
/note="52_copies 2 mer ct 78 conserved"
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                                   'note="MADE1 repeat: matches
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                                                                                                                       "L2 repeat: matches 2579.
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                                     23.
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8914. or
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13398. 13598
/note="AluSp repeat: matches 1.
13699. 13810
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complement(10179. 110678)
/note="match: GSS: Em:B56592"
complement(10204. 10728)
                                                                                                                                                  15490. .15662
/note="AluSg1 repeat: matches
15669. .15727
/note="MLTIB repeat: matches 1
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14868. .15040
/note="MIR repeat: matches 49.
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                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 141.
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18296. .183;
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14597. .15201
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13331. .13397
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12174. .12445
/note="L2 repeat: matches 1988
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10718. .11310
/note="match: GSS: Em:B14024"
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/note="AluJo repeat: matches 1.
   /note="MSTA repeat: matches
18324. .18392
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14368. .14452
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l3806. .13919
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                               Alux repeat: matches 1. .18323
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249. .10706)
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198545 bp
Homo sapiens chromosome 4 clone
SEQUENCE, 4 unordered pieces.
ACO17063
2 (bases 1 to 19 Waterston, R.H. Direct Submission
                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
1 (bases 1 to 198545)
Waterston, R.H.
                                                                               <u> Unpublished</u>
                                                                                                                  The sequence of Homo sapiens
                                                                                                                                                                                                                                                     Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Catarrhini; Hominidae
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                                                                                             Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On NOV 2, 2001 this sequence version replaced gi:15741601.
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Insert size: 200801; sum-of-contigs
Quality coverage: 10.58 in Q20 bases; agarose-fp
Quality coverage: 10.55 in Q20 bases; sum-of-contigs
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Sequencing vector: plasmid; 65%
Chemistry: Dye-primer ET; 34% of reads
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 happing Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                    ggaagaaatttctaagcagcaaagcattcaagaggtgacttgggtgctgtttaaaggcatt 450
                                                                                                                                                                                                                                        CAGTTTTATAAGGGAAACAGAGTATAAAAGTTTGAAAAATTTGCAGCCTGACAATGTGAT
                                                                                                                                                                                                                                                                                     | Cagtttcataagggaggcagagcataagagttcagaaaatttgcaccctgacaatgtgat 510
                                                                                                                          GGAAGACATTTCTAAGCAGAAAAGCATTCAAGAGGTGACTTGGGTACTGTTAGAGGCATC 66657
taatgaggagctgaatgttaatcctcaagacaatggggaaaatatctcctggacatgtca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               840;
                                                                                 VECTOR: PBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP11-279N8 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-279N8 is at 124518 in this sequence. The true left end of clone RP11-528D24 is at 114969 this sequence. The true right end of clone RP11-214011 is at 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr13
RP11-279N8 is from the library RPCI-11.1 constructed of Pieter de Jong. For further details see http://www.chori.org/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harnar/harna
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During sequence assembly data is compared from overlapping clones.
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R: pBACe3.6
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112388. .112496
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                                                               AL353634.4 GI:9863649
HTG; HTGS_PHASE2; HTGS_CANCELLED
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                                                                                                     Homo sapiens chromosome X clone RP11-435A2 map SEQUENCING IN PROGRESS ***, in ordered pieces.
                                       Homo sapiens
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692 gggacaggcccagggtccctgtgctgtgtgcagcctagagacttggtgccctgtgtccca
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Consensus quality: 76604 bases at least Q40
Consensus quality: 77098 bases at least Q30
Consensus quality: 77320 bases at least Q20
Insert size: 77405; sum-of-contigs
Insert size: 85298; 1.5% error; agarose-fp
Quality coverage: 4.54x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 21, 2000 this sequence version replaced gi:9213111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads
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Similarity 80.6%;
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/db_xref="taxon:9606"
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Submitted (22-FEB-1995) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humpub@sanger.ac.uk IMPORTANT: This sequence is the entire insert of clone U212C1. The true left end of clone U212C1 is at 1 in this sequence. The true right end of clone U212C1 is at 40714.

U212C1 is from the human chromosome X-specific cosmid library.
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 40714)
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/note="THE1B element fragment"
23725. .24279
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19720. .19797
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20518. .20734
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16651. .16712
/note-"THEIB element fragment"
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/clone_lib="LL0XNC01"
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/db_xref="taxon:9606"
 /note="THR element fragment"
24395. .24593
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16532. .16609
.note="THE1B element fragment"
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/note="THE1B element fragment"
16204. .16495
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                                                                                                      'note="MLT1A element fragment"
                                                                                                                                    'note-"MLT1A element fragment"
                                                                                                                                                                                                'note-"MER30 element fragment"
                                                                                                                                                                                                                                                            'note="MER21B element fragment"
                                                                                                                                                                                                                                                                                            'note="MER218 element fragment
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'note="L1 element fragment"
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                                                                           'note="THE1B element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                note="MSTC element fragment"
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te="L1 element fragment"
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Best Local Similarity 80.6%;
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                                                                                                                                    gtcttcacagcagtccatcaaatcactg-gcctggaggcctaggagaaaatggttttgtg
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                                                                                           ggacagggcccagggtccctgtgctgtgtgcagcctagagacttggtgccctgtgtcccag 752
                                                                           GGTCGGGCCCAGGGTCCCCATGCTATGTGCAGTCTAGGGACTTGGTGCCCCGTGTCCCAG
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24643 ...25270
/note="THR element fragment"
25277. ...25463
/note="THE1B element fragment"
25528...25627
/note="THE1B element fragment"
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/note="MER4B element fragment"

40640. .40693

/note="27 copies of 2 mer 94 % conserved"

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30032. .30159
/note-"MER5 element fragment"
31794. .31980
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28319. .28608
/partial
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/note="MSTC element fragment"
27949. .28241
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32232. .32735
note="MER9 element fragment"
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/note="LTR2 element fragment"
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'note="MLT1A element fragment"
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Pred. No. 1.8e-191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gagctgtgagaagaagtccaccatcctccagactccagaagggtagatccactgacagct 1079
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                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; (Mammalla; Eutheria; Primates; (1 chases 1 to 123070)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US On Jul 18, 2000 this sequence version replaced gi:7709316.
                                                                                                                                                                              2 (bases 1 to 123070)
DOE Joint Genome Institute.
Direct Submission
                                          Web site:
                                                          Center Code: JGI
                                                                              Center: Joint Genome Institute
                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        AC008799.4 GI:9256046
HTG; HTGS_PHASE2; HTGS_DRAFT.
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Homo sapiens chromosome 5 clone CTD-2061E19, WORKING
                                          http://www.jgi.doe.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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Best Local Similarity
Matches 853; Conserv
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Consensus quality: 121288 bases at least Q30
Consensus quality: 121288 bases at least Q30
Consensus quality: 122086 bases at least Q30
Consensus quality: 122086 bases at least Q30
Estimated insert size: 123000; pulse field gel estimation
Estimated insert size: 122770; sum-of-contigs estimation
Quality coverage: 6.05 in Q20 bases; pulse field gel estimation.
**NOTE: This is a 'working draft' sequence. It currently
** consists of 8 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** provided by the submittor.
** This sequence will be replaced
                                                                                                                                                        CCCATCATAAACCCCAAAGGCCTAGGAGAAAAGTGGTTTTGTGGGCCAGGCCCAGGGTC
                                                                            aagcattcaagaggtgacttgggtgctgttaaaggcattcagtttcataagggaggcaga 471
                    caaatcactggcctggaggcctaggagaaa---tggttttgtgggacagggccagggtc 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the accession number will be preserved.

1 9436: contig of 9436 bp in length
9437 9536: gap of unknown length
9537 26537: contig of 17001 bp in length
26538 26637: gap of unknown length
26538 46958: contig of 19321 bp in length
45959 46058: gap of unknown length
46059 68657: gap of unknown length
68658 68757: gap of unknown length
68658 68757: gap of unknown length
68758 72152: contig of 3995 bp in length
72153 7252: gap of unknown length
81169: contig of 8817 bp in length
81169: gap of unknown length
81170 121547: contig of 40378 bp in length
121548 121647: gap of unknown length
121648 121070: contig of 40378 bp in length
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Pred. No. 6.5e-191;
0; Mismatches 177;
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Indels

36; Gaps

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651

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Length 123070;

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REFERENCE
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,t Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Gage,D.
                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 2 clone SEQUENCE, 36 unordered miscon
                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                Unpublished
                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 2, clone RP11-792C1
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AC044889.2 GI:8016676
                                                                                                                                                                 (bases 1
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                                                                                                                                                                                   Chordata;
Primates;
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                                                                                                                                                                                     Hominidae;
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Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
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Stange-Thoman, N., Stolagovic, N., Suhramanian, A., Talamas, J.,
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Direct Submission
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Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731 Consensus quality: 168749 bases at least Q40 Consensus quality: 180047 bases at least Q30 Consensus quality: 184014 bases at least Q20 Insert size: 190000; agarose-fp Insert size: 196268; sum-of-contigs Quality coverage: 3.8 in Q20 bases; sum-of-cont Quality coverage: 3.9 in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L9594
Center clone name: 792_C_1
Center summary Statistics
Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT
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TITLE JOURNAL COMMENT

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is 13008 14917 15017 17115 1116 2285 2385 2389 3899 3999 5260 5360 1016 16 1115: gap of 100 bp of 2284: contig of 119 bp of 2284: contig of 1514 bp of 3898: contig of 1514 bp of 3998: gap of 100 bp of 5259: contig of 1261 bp of 5359: gap of 100 bp of 5259: contig of 1553 bp of 100 bp of 1701: gap of 100 bp of 1813: contig of 1133 bp of 100 bp of 17214: gap 18527: c 15016: gap of 100 bp 17114: contig of 2098 bp 17214: gap of 100 bp 11104: 12907: contig of 1803 bp 1 13007: gap of 100 bp 1 14916: contig of 1909 bp in 5016: gap of 100 bp 1 17114 1015: contig of 1015 b 115: gap of 100 bp 2284: contig of 1 : gap of 12907: 9694: contig of 1449 94: gap of 100 bp 11004: contig of 1210 þ đđ đđ ďď ď đđ nr dq bp in length 'n in 'n in 'n 'n in in in length length length length length length

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2485 22584: gap of 100 bp
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504 27703: gap of 100 bp
100 2703: gap of 100 bp
11 3020: contig of 2317 bp ii
12 30120: gap of 100 bp
21 33472: contig of 33472
73 33472: contig of 33472
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                                                                                                                                                                              5360.
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7013.
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                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-792C1"
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GCAGCTTCCATGTGGTGTTGAGCCTGCAAGTGCACAGAAGTCACAAATTGGGGTTTGGGA
                 gcagcttccaagtggtgttgagcctgtgggtgcaaagaagtcaagaattgaggtttgggg 855
                                                                                                                                                                                              cctgtgctgtgtgcagcctagagacttggtgccctgtgtcccagttaattca------
                                                                                                                                                                                                                                                                                       tcctcaagacaatggggaaaatatctcctggacatgtcagaggtcttcacaggcagtccat 651
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                                                                                  TGAAAGGGGCCAACATAGAGCTCGGGCTGTGGCTTCAGAAGGTGCAAGCCCCAAGCCTTG
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55363. .60982
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38185. 41069
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27704. .30020
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25388. .27603
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15017. .17114
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13008. .14916
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FEATURES Source

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Benton, J., Bilandge, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederlch, D.A., Delaney, K.R., Delyado, O., Denn, A.L., Ding, Y., Dinh, H. H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Dubbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Edwards, C., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Howard, S., Huber, J., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Hohnson, R., Jolivet, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L.C., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meddor, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Muzny, D., Neal, D., Nelson, D., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Newtson, S., Oguh, M., Okwonun, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Perez, L., Peters, L., Pickens, R., Primus, E., Payton, B., Peery, J., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Tamerisa, K., Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Vilalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlinams, G., Williams, G., Williamson, A., Sorrilla, S., Kucherlapati, R., Walson, D. and Gibbs, R.
                                     of Molecular and Human Genetics, Baylor College of Medicin
Baylor Plaza, Houston, Tx 77030, USA
On Aug 25, 2000 this sequence version replaced gi:9664948
INFORMATION: http://www.hgsc.bcm.tmc.edu/or email
                                                                                                                                             Direct Submission
Direct Submission
Submitted (25-AUG-2000) Human Genome Sequencing Center, Departmented (25-AUG-2000) Human Genetics, Baylor College of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                            Worley,K.C.
                                                                                                                                                                                                                                                                                                                                                                  Baylor Plaza, Houston, 3 (bases 1 to 154090)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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REFERENCE AUTHORS TITLE

JOURNAL TITLE

JOURNAL

REFERENCE TITLE JOURNAL AUTHORS

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome of a local database that includes entries Res. from 7:541-550) searches dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green

flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are identical matches are annotated as similar. unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons not

a region does not meet this standard, it will be indicated in SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence qualit as Low Coverage. quality for the and

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT-----

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                              complement(1248. .1584)
/rpt_family="MER468"
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                                                                                                                                                                                                                                 Location/Qualifiers
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             tgggagcccccacacagagtccccagtggggctccatctagtagagctgtgagaagaagt 1036
                                                                                                                                                               cctccaatcagatttcagaagatatatggaaacccctggatgcccaggcagaagtttgct
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TTGGAGCCCATACACAGAGTCCCTACTGGGGCACCATCTAGGGGAGCTGTGAGAAGAGGG
                                                                       TCAGGGGTGGGGCCCTCATGGAGAACCTCTGCTAGGGCAGTGCAGAAGGGAAATGTGGGG
                                                                                                                                               CCTCCACCTAGATTTCAGAGGATGTATGGAAATGCCTGGATGTCCAGGCAGAAGTTTGCT
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8113. .8267
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6571. .6616
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8666. .8695
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8385. .8587
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complement(6678...7
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5232. .5301
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            Muzny D. M., Admas C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Erieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Charles, M.C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delaney, K.R., Delado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delaney, K.R., Delaney, K.R., Delaney, K.R., Dederich, D.A., Delaney, K.R., Dederich, D.A., Delaney, K.R., Dederich, D.A., Delaney, K.R., Dinh, Y., Dinh, H.H., Delaney, K.R., Delaney, K.R., Dederich, D.A., Delaney, K.R., Dever, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Frantz, P., Garran, H., Havlak, P., Haves, A., Hernandez, J., Harris, K., Harris, H., Havlak, P., Haves, A., Hernandez, J., Harris, C., Harris, K., Harth, H., Havlak, P., Haves, A., Hernandez, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Jacobson, B., Haber, J., Hulyk, S., Hume, J., Jackson, L.E., Levis, C., Hulyk, S., Hume, J., Joudah, S., Jacobson, B., Huber, J., Hulyk, S., Hume, J., Joudah, S., Jacobson, B., Hulyk, S., Man, J., King, L., Levis, L., Lull, J., Liu, M., Loulseged, H., Liu, M., Loulseged, H., Liu, M., Loulseged, H., Lul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        actggatttcggacttatatggggcccgta-cccctttgtttttggccaatttttttccatt 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGGGTTTCAGACTTGCATGGGGCATATAGCCCCTTTGTTTTGGCCAATTTCTCCCATT 102613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccaccatcctccagactccagaagggtagatccactgacagcttgcagcatgtgcctgaa 1096
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Homo sapiens chromosome 12 clone RP11-307L1, WORKING DRAFT
SEQUENCE, 1 unordered pieces.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 186660)
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Svatek, A.,
Sparks,A., Stanley,H., Stone,H.
or,P., Tamerisa,A., Tamerisa,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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GCATAAACGTTTGGAAAATTTGCAGCCTGACAATGTGATAGAAAAAGAAAAACCCATTTTC 72022

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Matches 850
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                                                                                                            71843 GAACTTTGAACTTGAGAGACATGATTTAGGGTATCTGGCGGAAGAATTTCTAAGTAGCA 71902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                            412 aagcattcaagaggtgacttgggtgctgttaaaggcattcagtttcataagggaggcaga 471
                                                                                                                                            352 gaatatttggctaatgaggaagcaaattttggctaataaggaagaatttctaagcagca 411
850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-MAR-2000) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On May 1, 2001 this sequence version replaced gi:13877175.

Center: Baylor College of Medicine Center code: BCM
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Usman1,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.bgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                       57089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-primer Bodipy: 18% of reads
Chemistry: Dye-terminator Big Dye: 82% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 186630 bases at least Q40
Consensus quality: 186659 bases at least Q30
Consensus quality: 186660 bases at least Q30
Consensus quality: 1867779; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sgarose-fp estimation
Quality coverage: 10.7x in Q20 bases; sum-of-contigs estimation
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Center clone name: RP11-307L1
Center clone name: RP11-307L1
Center clone name: P11-307L1
Sequencing vector: Plasmid;
Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
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Location/Qualifiers
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/chromosome="12"
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Pred. No. 2.3e-190;
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                                                                                                                                                                                                                                                                                        ctggacgtgagacatggagtcaaaagagatcattttggagctttaagatttgactgcccc 1276
                                                                                                                                                                                                                                                                                                                                         aaaaccgtagtggcagagctgaccaagaccgtgggaatctacctcttgcattgtcatgac 1216
                                                                                                                                                                                                                                                                                                                                                                                         TCTGGGTTTCAGACTTGCATGGGGCATATAGCCCCCTTTGTTTTGGCCAATTTCTCCCCATT 72862
                                                                                                                                                                                                                                                                                                                                                                                                                                         ccaccatcctccagactccagaagggtagatccactgacagcttgcagcatgtgcctgaa 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGAGCCCATACACAGAGTCCCTACTGGGGCACCATCTAGGGGAGCTGTGAGAAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCCACCTAGATTTCAGAGGATGTATGGAAATGCCTGGATGTCCAGGCAGAAGTTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cagcttccaagtggtgttgagcctgtgggtgcaaagaagtcaagaattgaggtttgggaa 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAGGGGCCAGCATAGAGCTTGGGCCGTGGCTTCGGAGGGTGCAAGCCCCAAGCCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caaatcactggcctggaggcctaggagaaaatggttttgtgggacaggcccagggtccct 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGGGGAATTTGAAGCTGGCTGCAGAAATTTGCATAAGTAACAAGGAGCCTAATGTTAA 72082
                                                                                                                                                                                                                                                                          CTAGATGTGAAACATGCAGTCAAAGGAGATCATATTAGAACTTTGAGATTTGACTACCCT 72802
                                                                                                                                                                                                                                                                                                                          AAAGCCACAGAAGCAGAGCTTCCCAAGACCATGGGAACCCACCTCTTGCATCAGTGTGAC
                                                                                                                                                                                                                                                                                                                                                                             AAAGCCACAGAGACTCAACACCAGCCCATGAAAGCAGCCAAGAGGGAGCCTGTACCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                           CCACCATCCTCCAGACCCCCAGAATGGTAGATCCACCAACAGCTTGCACCATGTACCTGGA 72622
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                                                                         Homo sapien
AC091982
AC091982.3
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 170368)
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                                                                                                 sapiens chromosome
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   Drive, Walnut Creek, CA 94598, USA
on Aug 23, 2001 this sequence version replaced gi:11079410.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                 Submitted (23-AUG-2001) DOE Joint Drive, Walnut Creek, CA 94598, USA
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Drive, Walnut Creek, CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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atgttgggtgggagccccacacagagtccccagtgggctccatctagtagagctgtga 1028
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tgcctgaaaaatccacagacactcagtgccagcctgtgaaagcagcagggatggagtctg
                                                                                                                                                                                                                                                           agtttgctgtaggggtgggggtcctcatggagaacctctgcaagggtagtacaaaagggaa
                                                                                                                                                                                                                                                                                                                                                tttgggaacctccaatcagatttcagaagatatatggaaacccctggatgcccaggcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                     agccttggcagcttccaagtggtgttgagcctgtggggtgcaaagaagtcaagaattgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGGTCCCTGTGCTGTGCGGTCTAGAGACTTGGTGCCCTGTGTCCCAGCCACTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agcagtccatcaaatcactggcctggaggcctaggagaaaatggttttgtgggacaggcc
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                                                                                                                                                                                                                                                                                                                            TTTGGTAACCTCTGCCTAGATTTCAGAAGGTGTATGGAAACCCCTGGATGCCCAAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCTTGGCAGCTTCCACGTGGCATTGAGCCTGCGGGCGCACAGAAGTCAAGAATTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATGACTAAAAGGTGCCAAAGTACAATTCAGGTTGTTTCTTCAGAAGGTGGAAGCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCAGCCACTCCCATCACAGGCCCAAAGGCTTTGGAGAAAATCGTTTCGTGGGCCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCCATTTTCTGAGGAGAATTGAAGCCAGCTGAAGAATTTGCATAAGTAATGAGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAAGCAGAGCATAAAAATTTGGAAAATTTTGCAGCCTGACAATGTGCTAGAAAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finishing Completed at Stanford Human www-shgc.stanford.edu Quality: Phrap Quality >=40 99.7% of Sestimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHGC-10855 G13672
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/chromosome="5"
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1. .67984
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Pred.
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No. 1.6e-189;
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REFERENCE
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ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., McPheters, R., Meldrim, J., Meneus, L.,
Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Petterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N.,
Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, E., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTGTGACCTGCATATGAGACGTGGAGTCAAAAGAGATCATTTTGGATCTTTAAGACTTG
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                                                                                                                                                                                                                                                                                                                                                   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,B., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Gilnde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
                            McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
                                                                                                                                                                                      Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 168502)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome AC091005
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC091005.9
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    Rieback, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168502 bp DNA linear PRI 11-DEC-200 ne 15, clone RP11-1008C21, complete sequence.
                                                                                                                                                                                                                                                                                                                  Hulme, W., Iliev, I., Johnson, R.,
    Riley, R., Rise, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 11, 2001 this sequence version replaced gi:15412474. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Center clone name: 1008_C_21
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Ouery Match 804; Conservative 0.3%; Score 684; DB 9; Length 168502; Best Local Similarity 0.3%; Pred. No. 55-8189; Oy 322 abatatrugarealyes 0; Mismatches 175; Indels 35; Gaps 471 ACCANTONACTROANCEMANDAMENTAMENTAMENTAMENTAMENTAMENTAMENTAMENT
Best Local Similarity 49.5%; Score 664; DB 9; Length 168502; Rectional Stanilarity 80; State 168502; Matches 844; Conservative 0; Hismatches 175; Indels 35; Gaps Matches 844; Conservative 0; Hismatches 175; Indels 35; Gaps Matches 844; Conservative 0; Hismatches 175; Indels 35; Gaps 1846; Conservative 0; Hismatches 175; Indels 35; Gaps 1846; Conservative 0; Hismatches 175; Indels 35; Gaps 1846; Conservative 1

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Direct Submission Unpublished 2 (bases 1 to 73390) Worley.K.C. Direct Submission Submitted (19-0cT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 73390) Worley.K.C. Direct Submission Submitted (01-JAN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 1, 2001 this sequence version replaced gi:11138159.	Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bhhay, C., Burcht, S., Burcht, C., Burcht, K., Bydd, N.C., Chern, G., Chen, R., Chen, G., Chen, G., Chen, G., Chen, G., Chen, G., Chen, C., Coyle, M.D., Datborne, S.R., David, R., Davila, M.L., Davis, C., Cox, C., Coyle, M.D., Datborne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Drayer, H., Davis, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguro, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguro, D., Elhay, C., Emerling, S., Escotto, M., Falls, T., Ferraguro, D., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguro, D., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Falls, T., Garza, M., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Harris, C., Harris, J., Harris, C., H	Mammalia: Butheria; Prinates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 73390) Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,	ACO12038 ACO

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation html.

QUALSTAT-REPORT-----

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complement(17251. .17555)
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/rpt_family="L2"
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/rpt_family="MSTA-internal"
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GAATGGCTGTATTTACTCAATACCTGTACCCCCATTGTATCTAG
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Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Sep 5, 2001 this sequence version replaced gi:15209227.

On Sep 5, 2001 this sequence version replaced gi:15209227.
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Submitted (04-SEP-2000) Genome
University School of Medicine,
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The sequence of Homo sapiens BAC clone RP11-42414
Unpublished (2001)
                                                                                                                                                                                           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Submitted (05-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
The clone sequenced to the left is RP11-22L19, 2000 bp overlap; to clone sequenced to the right is RP11-364I15. Actual start of thi clone is at base position 188335 of RP11-22L19; actual end is at base position 131215 of RP11-424I4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ing information for this clone was provided by Dr. John D. erson, Department of Genetics, Washington University, St. 1 For additional information about the map position of this
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8317. .85
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299. .594
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873. .916
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5132. .5339
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/rpt_family="MIR"
10647. .10943
                                /rpt_family="AT_rich"
10278. .10489
                                                                                                                                   8908. .8938
                                                                                                                                                                    /note="match to EST AW899791 (NID:g8063996)"
8908. .8923
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/db_xref="taxon:9606"
/chromosome="2"
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/rpt_family="Alu" 11723. .11855

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                                                  TAATGAGGACCCGAATGTTAATCCCCCAAGACAATGGGGGAGAATGTCACCAGGACATGTCA
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11870. .11997
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11995. .12182
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20757. .20793
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15447. .15484
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25878. .27380
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24692. .24726
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19931. .20459
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12242. .12907
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5. .22891
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                                                                                Eukaryoia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 173480)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiquenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                    CNSOOM8T 173480 bp DNA linear PRI 04-MAY-2001
Human chromosome 14 DNA sequence BAC R-483C6 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
 Submitted (04-MAY-2001)
BP 191 91006 EVRY cedex
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                            Direct Submission
                                          Genoscope
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National de Sequencage
segref@genoscope.cns.fi
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Best Local Similarity 81.7
Matches 839; Conservative
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Assembly program: F
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n Apr 19, 2000 this sequence version replaced gi:7413814.
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/clone="R-483C6"
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Search completed: June 30, 2002, 14:50:15 Job time: 8882 sec

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6 095495
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09n178 sus scrofa
095j95 canis famil
095m94 bos taurus
090wb3 brachydanio
09bxj2 homo sapien
095jd7 macaca mula
062789 sus scrofa
096h05 homo sapien
                                                                                     Q96pm8 homo sapien
Q920n0 tamias sibi
Q9h7z0 homo sapien
Q9z1k4 rattus norv
Q96d07 homo sapien
Q96np0 homo sapien
Q96d2v4 mus musculu
Q92188 mus musculu
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4.0	4.0	4.0	4.0	4.0	4.1	4.2	4.2	4.3	4.4	4.4	4.4	4.4	4.4	4.4	4.4	.5 .5	4.5	5	4.7	4.7	4.8	4.9	4.9	5.0	5.1	5.2	5.2	ა
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Q9EQZ7	Q9QZZ9	Q9UKV3	075158	Q9UPU6	Q9DCM6	Q91ZU6	д9вхJ3	Q9P2A5	Q9D0W2	Q9DCB6	Q9QYX7	Q9QYX6	015048	Q50279	Q96Н17	Q9QX74	Q03306	077782	Q96NW7	Q9P2I2	09вхJ5	09вхл0	Q9UFX4	Q9D8U4	Q99NE5	Q9JIR4	035168	Q96DL2
Q9eqz7 mus musculu	Q9qzz9 rattus norv	homo		Q9upu6 homo sapien	mus	6 mus	homo	Q9p2a5 homo sapien	Q9d0w2 mus musculu	Q9dcb6 mus musculu	Q9qyx7 mus musculu	mus	O15048 homo sapien	Q50279 mycoplasma	Q96h17 homo sapien	Q9qx74 rattus norv	Q03306 saccharomyc	oryc	homo	homo	homo	homo	Q9ufx4 homo sapien	mus	Q99ne5 mus musculu	Q9jir4 rattus norv	æ	Q96dl2 homo sapien

ALIGNMENTS

RESULT Q920NO ID Q AC Q DT 0	Оу ДЬ Оу	Que Bes Mat	RA RT OF RES	200000000000000000000000000000000000000	RESULT Q96PM8 ID Q
LT 2 NO Q920NO PRELIMINARY; PRT; 196 AA. Q920NO; Q1-DEC-2001 (TrEMBLrel. 19, Created)	255 VASEGASPKPWQLPSGVEPVGAKKSRIEVWEPPIRFQKIYGNPWMPRQKFAVGVGSSWRT 314	Query Match 17.1%; Score 427; DB 4; Length 130; Best Local Similarity 72.2%; Pred. No. 4.8e-31; Matches 83; Conservative 6; Mismatches 26; Indels 0; Gaps	SEQUENCE FROM N.A.; SEQUENCE FROM N.A.; Lu X., Cui L., Li Y.; "Human B Lymphocyte Activation-related Gene."; "Human B Lymphocyte Activation-related Gene."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF304442; AAL26787.1; SEQUENCE 130 AA; 14001 MW; 91BD443E8E0FFAC4 CRC64;	01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) B LYMPHOCYTE ACTIVATION-RELATED PROTEIN BC-1514. Homo sapitens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606;	JLT 1 W8 W8 PRELIMINARY; PRT; 130 AA. OGEDW8:

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RESULT OPH7200 QX.
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Q9H7ZO;
Q1-MAR-2001 (TrEMBLrel. 16, Careated)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-CT-2001 (TrEMBLrel. 18, Last annotation update)
Q1-CT-2001 (TrEMBLrel. 18, Last annotation update)
Q1-CT-2001 (TrEMBLrel. 18, Last annotation update)
Q1-CT-2001 (TrEMBLrel. 18, Last sequence update)
Q1-CT-2001 (TrEMBLrel. 18, Last sequence update)
Q1-CT-2001 (TrEMBLrel. 16, Last sequence update)
Q1-CT-2001 (TrEMBLrel. 18, Last sequence update)
Q1-CT-2001 (TrEMBLrel. 18
                                                                                                                                                                                                                                                                                                                                                                                              ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Negai K., Sugano S., Takahbashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; NEDO human CDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK024120; BAB14833.1; -. 64EED514F9F541D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ono M., Hosoe Y., Azuma Takamatsu N.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAIFYLMYNVLNDQVSCSGPPGPVGYPGVPGVPGPRGPPGQPGAAGRPGDPGPKGPSVKC
                                                                                                                                                                        RPR----RKWFCGTGPGS--LCCVQP-----RDLVPCVPVNSAVASEGASPKPWQLPSGV 271
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                                                                                                       RPRGLGGKDDFMGQALGSPALCRLQTWYPAFQKLQPC--LKEAKVQLGF---
                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                             Conservative
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21330 MW;
                                         KKSRIEVWEPPIRFQKIYGNPWMPRQKFAVGVGSSWRTSARVVQK
                                                                                                                                                                                                                                                                         11.0%;
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    Last sequence update)
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                                                                                                                                                                                                                                                                         Score 275;
Pred. No. 6.
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Pred. No. 1.
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.9e-21;
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Best Local
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EMBL; AJ131848; CAA10518.1; -.

InterPro; IPR001073; C1g.

InterPro; IPR001087; Collagen.

Pfam; PP00386; C1g 1.

Pfam; PP01391; Collagen; 2.

PRINTS; PR00007; COMPLEMNTC1Q.

SMART; SM00110; C1g; 1.
Q96D07;
Q96D07;
01-DEC-2001
01-DEC-2001
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Q9Z1K4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created 01-MAY-1999 (TrEMBLrel. 10, Last sec 01-DEC-2001 (TrEMBLrel. 19, Last and COLLAGEN ALPHA 1 TYPE X (FRAGMENT).
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STRAIN-SPRAGUE-DAWLEY;
MEDLINE-20310874; PubMed-10853827;
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Mammalia; Eutheria;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGPPGRPGPRGHTGEPGLPGPPGPPGPPSQAVIPDGFTKSGQRPRLSGMPLVSANQG
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QGIGSFHGVLSLQGHRSQLLRLGNLHLDFKRCMEMPDDQAEVCCIG-GPSWRTSARAVWK
                                                                                                                                                                                                   NGLYSSEYVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGPPAHPRPPEEVGPPGAPGLPQYTGEISEMTKCPCPD-----
                                                                                                                                                                                                                                                                                             KGTHVWVGLYKNGTPTMYTYDEYSKGYLDQASGSAIMELTENDQVWLQLP-----
                                                                                                                                                                                                                                                                                                                                                                                          VTGMPVSAFTVILSKAYPAVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHIHV
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Rodentia;
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Pred. No. 3.
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Sciurognathi; Muridae;
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.7e-07;
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                  Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamzaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Sato K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B. Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O96NPO;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
CDNA FLJ30449 FIS, CLONE BRACE2009274.
                                                                                                                                                                                             "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; AK055011; BAB70839.1; -
SEQUENCE 216 AA; 23140 MW; 976A49B029A84D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2001) to the EMBL; BC013581; AAH13581.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-LUNG CARCINOMA;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 744 AA; 73364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 73.4 KDA PROTEIN. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                TISSUE-CEREBELLUM;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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                            256
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72
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                            ASEGASPKPWQLPSGVEPVGAKKSRIEVW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQPGLPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYGAKKGKNGGPAY
                                                                                     CQRSSQQSIKSLAWRP----RRKWFCG--TGPGSLCCV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPPAHPRPPEEVGPPGAPGL----PQYTGEI------SEMTKCPCPDI 56
                                                       CQRSSW----LPLQYRPGGLRGKNGFMGQSQSPAANCILGTWCPASQPLQLQLWLWLKGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VNIWLMRKQILANKEEI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHV---HCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELHHCK 116
                                                                                                                                   Similarity
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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PWLQRVQATSLGGFHMVLGLWVHKRQERRFGSLHLDFRGCMEMPGCPGRTPL
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                                                                                                                 Score 158; DB
Pred. No. 2.4e
19; Mismatches
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Pred. No. 5.1e-06;
                                                                                                                                                                                               976A49B029A84D36 CRC64;
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                                                                                                                                   .4e-06;
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                                                                                                                                              Length 216
                                                                                   -QPRDLVPCVPVNSAV
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                          -----EPPI 288
                                                                                                                                                                                                                                                                      Kawakami B.,
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
Ra Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
Ra Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuchi R., Chido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Bustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ra Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ra Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Hayashtyaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).

EMBL; AKO18742; BAB31383.1; -.

MGD; MGI:88463; CO18a1

InterPro; IPR0001073; C1q.

InterPro; IPR00087; Collagen.

Pfam; PF01391; Collagen; 7.

PRINTS; PR00007; COMPLEMNTC10.
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Q9D2V4;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0007; COMPLEMNTC1Q
SMART; SM00110; C1Q; 1.
PROSITE; PS011113; C1Q; 1.
SEQUENCE 744 AA; 73581 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001
01-JUN-2001
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROCOLLAGEN,
                                                             615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection.";
     117
                                                                                                                                                                         555
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                                                                                                               58
                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                Local Similarity
VNIWL 121
                                                             MPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHV--
                                                                                                                                                                                                                        GPPAHPRPPEEVGPPGAPGL---PQYTGE-----
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                                                                                                                                                                         GQPGLPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGVKPPHAYAGKKGKHGGPAYE
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Rodentia;
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32.0%;
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17, Last annotation updat
ALPHA 1.
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Sciurognathi;
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                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                157.5;
No. 1.4
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chi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                .4e-05;
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                                                                                                                                                                                                                              -----ISEMTKCPCPDIE 57
                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                     25;
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suki S.,
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                                                                                                                                                                                                                                                                                  Gaps
                                                             671
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Best Local :
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Q921S8;
01-DEC-2001 (TEMBLrel. 19, C
01-DEC-2001 (TEMBLrel. 19, L
01-DEC-2001 (TEMBLrel. 19, L
                                   "Abnormal growth plate function in pigs carrying a dominant mutation in type X collagen.";
Mamm. Genome 1:1087-1092(2000).
EMBL; APZ22861; AAF37271.1; -.
InterPro: IPR001073; C1q.
InterPro: IPR001073; Collagen.
Pfam; PP01385; C1q; 1.
Pfam; PP01391; C011agen; 6.
PRINTS; PR00007; COMPLEMNTC1Q.
SWART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC011061; AAH11061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                 Nielsen V.H., Bendixen C., Arnbjerg J., Shukri N.M., Thomsen B.;
       SEQUENCE
                         Collagen
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-21015405; PubMed-11130976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9N178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROCOLLAGEN, TYPE VIII, ALPHA 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 MPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHV---HCKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 VNIWL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 GQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGVKPPHAYAGKKGKHGGPAYE 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GPPAHPRPPEEVGPPGAPGL---PQYTGE------ISEMTKCPCPDIE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 32.0
40; Conservative
       675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73621 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
       65447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.0%;
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15,
    XX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 157.5; DB 1
Pred. No. 1.4e-05;
4; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF7A7FD79D8463AA CRC64;
  26397B10310383F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               675
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                                                                                                                                                                                                                                                                                                                           Sorensen C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                             Jensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                           H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Best Local S
Matches 45
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Q95J95;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q.
Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                              Q95MQ4
Q95MQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dea M.K., Bergman R.N.;
"Regulation of Adiponectin gene
Submitted (SEP-2001) to the EMBI
EMBL; AF417206; AAL09702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-ADIPOSE TISSUE;
MEDLINE-21369933;
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADIPONECTIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 WVGLYKNGTPVMYTYDEYVK 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 KVNIWLMRKQILANKEEISK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 GPPGAPGLPQYTGEISEMTKCPCPDIERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTGKFHCNIPGLYYFSYHITVYLKDVKVSLYKKDKAMLFTYDQYQEKNVDQASGSVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAMGVFACRVPGNYYSSF--DVELHHCKVNIWLMRKQILANKEEISKQQSIQEVTWVLL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SAFTVILSKAYPAIGAPIPFDKILYNGQQHYDPKTGIFTCRIPGIYYFSYHIHVKGTHA 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELH--HC 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TremBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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     PubMed=11382781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20890 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s.,
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; Pred. No. 1.4e-05;
14; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 155.5; DB v;
Pred. No. 3.5e-06;
                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression in EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ionut V.,
                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3AA3D947D187AF9A CRC64;
                                                                                                                                                                                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fat-fed
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                                                                                                                                Bovoidea
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RESULT OPOMB3
ID WB3
ID WB3
ID WB3
ID WD7
ID 01:
DT 01:
DT 01:
DT 01:
DT 02:
DT
   RESULT
Q9BXJ2
ID Q9
AC Q9
DT 01
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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EMBL; AFE99230; AAKS8902-1; -
EMBL; AFE99230; AAKS8902-1; -
EMBL; AFE99230; AAKS8902-1; -
C6253BA803B9A668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lieschke G.J., Oates A.C., Crowhurst M.O., Ward A "Morphological and functional characterization of macrophages in embryonic and adult zebrafish."; Blood 0:0-0(2001).
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Pred. No. 3.4e
L2; Mismatches
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Pred. No. 4.7e-06;
7; Mismatches 64
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"Homo sapiens complement-clq tumor necrosis factor-related pro
L Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

R InterPro; IPR001073; C1q.

R InterPro; IPR000087; Collagen.

R Pfam; PF00386; C1q; 1.

R Pfam; PF01391; Collagen; 1.

R Pfam; PF01391; Collagen; 1.

R PRINTS; RR000107; CONPLEMNTC1Q.

R SMART; SN00110; C10; 1.

R PROSITE; PS01113; C10; 1.

SEQUENCE 289 AA; 30683 MW; A61609FF86D26946 CRC64;
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Q95JD7;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                   TISSUE-ADIPOSE TISSUE;

MEDLINE-21232234; PubMed-11334417;

Hotta K., Funahashi T., Bodkin N.L., Ortmeyer H.K., Ari
Hansen B.C., Matsuzawa Y.;

"Circulating concentrations of the adipocyte protein ad
decreased in parallel with reduced insulin sensitivity
progression to type 2 diabetes in rhesus monkeys.";
Diabetes 50:1126-1133(2001).

EMBL; AF404407; AAK92202.1; -.

SEQUENCE 243 AA; 26264 MW; 49A45DAF2B4613FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (Rhesus macaque)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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etazoa; Chordata;
theria; Primates;
- IERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYY
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Pred. No. 6.7e
11; Mismatches
                                                                                                             Score 140.5;
Pred. No. 0.00
7; Mismatches
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                                                                                                                              140.5;
No. 0.0
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No. 6.7e-05;
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RESULT 15
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SIGUENCE FROM N.A.

TISSUE-ARATIC SMOOTH MUSCLE;

A Reichenberg S., Plenz G., Robenek H.;

Reichenberg S., Plenz G., Robenek H.;

Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

E Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

R PERL, AF054891, AAC08999.1; -.

R PHIL, AF054891, AAC08999.1; -.

R Pfam, PF00386; C1q; 1.

R PRINTS; PR00007; COMPLEMNTC1Q.

R PRINTS; PR00110; C1Q; 1.

R PROSSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.5%; Score 137; DB 6; Length 173; Best Local Similarity 30.3%; Pred. No. 0.00014; Matches 37; Conservative 18; Mismatches 45; Indels 22;
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O62789;
O1-AUG-1998 (TIEMBLTE1. 07, Created)
O1-AUG-1998 (TIEMBLTE1. 07, Last sequence update)
O1-JUN-2001 (TIEMBLTE1. 17, Last annotation update)
COLLAGEN VIII (FRAGMENT).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID-9823;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                7 PPPHGEYLPDMGLGIDGAKPPHAYG-----AKKGKNGGPAYEMPAFTAELTAPFPPV 58
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173 AA; 18973 MW;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 30, 2002, 11:52:24; Search time 13.41 Seconds (without alignments) 1325.300 Million cell updates/sec

Perfect score: Sequence: US-09-997-610-2 2494 1 IVVIPVLITAVIEHVEVAGP......GOFFPFGTAVFTQCLYLHCM 459

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB : Maximum DB : seq length:
seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

332333103300000000000000000000000000000	Result No.
233 221 167.5 165.5 163.5 159.5 159.5 159.5 159.5 1146.5 1146.5 1146.5 1146.5 1146.5 1146.5 1147.5 1149.5 110.5 11	Score
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196 215 215 216 674 744 680 674 680 680 670 247 247 247 248 255 255 255 255 255 255 255 255 255 25	Length DB
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ALIGNMENTS

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BAA02351.1; 0001073; C1q. 0000087; C011a ; C1q; 1. 07; COMPLEMNT 0; C1Q; 1. 113; C1Q; 1.	between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).		ibernation."; Biol. Chem. 267:473-478(1992). 1- FUNCTION: PLASMA PROTEINS HP-20, HP-2 140 kDa COMPLEX VIA DISULFIDE BONDS I HIBERNATION SPECIFIC. 1- SUBCELLULAR LOCATION: Extracellular.	SEQUENCE OF 24-58; 66-99; 104-129; 132-136 AND 150-184. TISSUB-Plasma; MEDINE-92112996; PubMed-1730610; Kondo N., Kondo J.; "Identification of novel blood proteins specific for mammalian	NCBI_TaxID=64680; [1] SEQUENCE FROM N.A. TISSUE=Liver; TISSUE=Liver; Takamatsu N., Ohba K., Kondo J., Kondo N., Shiba T.; Takamatsu N., Ohba K., Kondo J., Kondo N., Shiba T.; "Hibernation-associated gene regulation of plasma proteins with a collagen-like domain in mammalian hibernators."; Wol. Cell. Biol. 13:1516-1521(1993).	RESULT 1 ID HP20_TAMSI STANDARD; PRT; 196 AA. AC Q06575; DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 01-MAR-2002 (Rel. 41, Last annotation update) DE Hibernation-associated plasma protein HP-20 precursor (Hibernator- DE specific blood complex, 20 kba subunit). OS Tamias sibirious (Siberian chipmunk) (Asian chipmunk). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

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14P25_TAMSI STANDARU,
2 Q06576;
3 Q06V-1995 (Rel. 32, Created)
31-NOV-1995 (Rel. 32, Last sequence)
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Best Local S
Matches 69
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01-MAR-2002 (Rel. 41, Last annotation update)
Hibernation-associated plasma protein HP-25 precursor (
specific blood complex, 25 kDa subunit).
Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
Eukaryota, Metazoa; Choddata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                the
                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kondo N., Kondo J.;
"Identification of novel blood proteins specific hibernation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 29-62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=64680;
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                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 267:473-478(1992).
- FUNCTION: PLASMA PROTEINS HP-20, HP-140 KDa COMPLEX VIA DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LAIFVLMVNVLNDQVSCSGPPGPVGYPGVPGVPGPRGPPGQPGAAGRPGDPGPKGPSVKC
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                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Extracellular.
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
DEVELOPMENTAL STAGE: THE PROTEIN COMPLEX DISAPPEARS FROM
PLASMA AT ONSET OF HIBERNATION AND REAPPEARS AS HIBERNATI
                                                                           ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                 SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                     CEASES
                                                                                                                                                                                                                                                                                                                                                               HIBERNATION SPECIFIC
                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its content of the second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYHCKVKIGLMKNHIQVMEKHQLSKNE 151
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Pred. No. 3.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C10.
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THE PLASMA AND AR
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                                                                                                                                                                                                                                                          HIBERNATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                       ARE
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                                                                                                        collaboration
L outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вр
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRODOOT; COMPLEY SMART; SM00110; C10; 1. PROSITE; PS01113; C10;
                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                     collagen polypeptide and are expressed by valendothelial and mesenchymal cells in newborn Eur. J. Biochem. 207:895-902(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.
                                                                                                                                                                                                                            Ninomiya Y.;
                                                                                                                                                                                                                                                     MEDLINE=92362626;
                                                                                                                                                                                                                                                                    STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                           Collagen alpha 1(VIII) chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q00780;
                                                                                                                                                                                                                                                                                                                                                                                                                                              CA18_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Collagen; Glycoprotein; Plasma; Multigene family. SIGNAL 1 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D12975; BAA02352.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               "Alpha 1(VIII)-collagen
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                             FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION
                        SIMILARITY: STRONG, TO ALPHA 2 TYF
SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                     PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
                                                                                                      WITH ALPHA 2(VIII) TYPE COLLAGENS.
TISSUE SPECIFICITY: HIGH LEVELS IN CALVARIUM,
                                                                           NEWBORN MICE; ALSO IN VARIOUS MESENCHYMAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELHHCKVNIWLMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGIQVREKEAQANDSYKHAMGSVIMALGKGDKVWLESKLKGTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQILANKEEI----SKQQSIQEVTWVLLKAFSFIREAEHKSSEN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLSERPPEPFQPIVFKEALYNQEGHFNMATGEFSCVLPGVYNFGFDIRLFQSSVKIRLMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPCGPPGPPGPPGIPGFPGAPGALGPPGPPGVPGIPGPQGPPGDVEK---CSSRPKSAFAV
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57; Conser
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83
167
215 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMNTC1Q
                                                                                                                                                                                                                                       PubMed=1499564;
ta C., Inoue M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
215
167
                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22664 MW;
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                                                                                                                                                                                                               gene transcripts encode a short-chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 221; DB 1;
Pred. No. 6.8e-10;
0; Mismatches 69;
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, AFE03206917EA530 CRC64;
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                                                                                        EPITHELIAL,
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ewborn mouse tissues.";
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                                                                                           ENDOTHELIAL
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Best Local S
Matches 51
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Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 7.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                    /_TAMSI
HP27_
                                                                                                                                    O06577;
O1-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
O1-MAR-2002 (Rel. 41, Last annotation update)
Hibernation-associated plasma protein HP-27 precursor (H
specific blood complex, 27 kDa subunit).
Tamlas sibiricus (Siberian chipmunk) (Asian chipmunk).
Tamlas sibiricus (Siberian chipmunk) (Asian chipmunk).
                                                                                                                                                                                                                                                     HP27_TAMSI
Q06577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extraceilular matrix; Connective tissue; Repeat; Hydroxyla Glycoprotein; Cell adhesion; Collagen; Signal. SIGNAL 1 28 BY SIMILARITY; CHAIN. 29 743 COLLAGEN ALPHA 1(VIII) CHAIN. DOMAIN 29 117 NONHELICAL REGION (NC2). DOMAIN 572 743 NONHELICAL REGION (NC1).
MEDLINE=93180798; PubMed=8441393; Takamatsu N., Ohba K., Kondo J., Kondo N., Shiba Takamatsu N., Ohba K., Kondo J., Kondo N., Shiba Takamation-associated grapulation of plasma collagen-like domain in mammalian hibernators."; Mol. Cell. Biol. 13:1516-1521(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X66976; CAA47387.1; -.
EMBL; X66977; CAA47387.1; JOINED.
PIR; S23779; S23779.
                                                                                 TISSUE-Liver;
                                                                                                                     NCBI_TaxID-64680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:88463; Col8a1.
InterPro; IPR001073; Clq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPAHPRPPEEVGPPGAPGL---PQYTGE-ISEM-----TKCP-----CPDIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 6.9%;
l Similarity 27.4%;
51; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-
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118
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117 N
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73595 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 171; DE Pred. No. 1.8e 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C1Q.
; 350E29502653EE0B CRC64;
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                    215
                                                                                                                                                                                                                                                                                                                                                                                     ----GFLDQASGSAVLLLRPGDQVFL
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.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                   ₽
                                                                                                                                                                                                 precursor (Hibernator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 743;
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                                        proteins
                                                                                                                                                          Euteleostomi;
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                                        with
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CA1A_CHICK
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                                                                                                                                                                                                                                                                                                                         Query Match
                               P08125;
01-AUG-1988 (Rel. 0
01-NOV-1991 (Rel. 2
15-JUL-1999 (Rel. 3
Collagen alpha 1(X)
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
SIGNAL
Eukaryota;
           Gallus gallus (Chicken).
                                                                                            CA1A_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00007; COME SMART; SM00110; C1Q;
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InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of novel blood proteins hibernation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92112696;
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D12976; BAA02353.1; -.
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                                                                                                                                                         133 GLYQFGFHIEAVQRAVKVSLMRNGTQVMEREAEAQDGYEHIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIBERNATION SPECIFIC.
SUBCELLULAR LOCATION: Extracellular.
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
DEVELOPMENTAL STAGE: THE PROTEIN COMPLEX DISAPPEARS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Siol. Chem. 267:473-478(1992).
FUNCTION: PLASMA PROTEINS HP-20, HP-
140 kDa COMPLEX VIA DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEASES
                                                                                                                                                                               GNYYSSFDVELHHCKVNIWLMRKQILANKEEISKQQSIQEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMA AT ONSET
                                                                                                                                                                                                                                                      ILALSVLMHVVCSETQGNPESCNVPGPQGPPGMRGPPGTPGKPGPPGWNGFPGLPGPPGP 77
                                                                                                                                                                                                                             TGEISEMTKCPCPDIERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PS01113; C10; 1.
Collagen; Glycoprotein; Plasma; Multigene family.
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF 31-215.
Metazoa;
                                                                                                                                                                                                      -MT-VNCHSKGTSAFAVKANELPPAPSQPVIFKEALHDAQGHFDLATGVFTCPVP
                                                                                                                                                                                                                                                                                                                                                            43
83
155
41
41
51
                                                                                                                                                                                                                                                                                                    Conservative
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                                   1(x)
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                                 . 08, Crea
. 20, Last
. 38, Last
(X) chain
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215
155
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51
22797
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 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF HIBERNATION
                                                                                                                                                                                                                                                                                                               6.7%;
31.5%;
                                             Last sequence update)
                                                                      Created)
                                                                                                                                                                                                                                                                                                  %; Score 167.5;
%; Pred. No. 7.5e
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                               ¥.
                                   precursor
                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC.
V -> A (IN REF. 2
R -> Q (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                    HP-27
                                                                                                                                                                                                                                                                                                                                                                                                                                              HIBERNATION-ASSOCIATED PLASMA PROTEIN
Craniata;
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                              -> A (IN REF. 2).
-> Q (IN REF. 2).
D2357086A088FA9E
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 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific
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les 68;
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                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                               CRC64;
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                                                                                                                                                                                                                                                                                                   Gaps
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Matches
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MOD_RES
SEQUENCE
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Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;

"The cloning and sequencing of alpha 1(VIII) collagen cDNAs

demonstrate that type VIII collagen is a short chain collagen and

contains triple-helical and carboxyl-terminal non-triple-helical

domains similar to those of type X collagen.";

J. Biol. Chem. 264:16022-16029(1999).

-i- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC

CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE

MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A31896; A31896.
InterPro; IPRO01073; C1q.
InterPro; IPRO01087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M13496; AAA48736.1; ALT_SEQ. EMBL; J04194; AAA48634.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luvalle P., Ninomiya Y., Rosenblum N.D., Ols "The type X collagen gene. Intron sequences region and separate the coding regions for t terminal and triple-helical domains.";
J. Biol. Chem. 263:18378-18385(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        open
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE MEDLINE=86168227; PubMed=3082876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
[1]
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                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                            Cartilage;
                                                                                                                                                                                                                                                                                                                                             Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01113; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-75 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The developmentally regulated type open reading frame without introns."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ninomiya Y., Gordon M., van der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89380199; PubMed=2476437;
  18
                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
AGPPAHPRPPEEVGPPGAPGLPQ--YTGEISE--
                                                                                                                                                                                                                                                                                                                                                                                    SM00110; C1Q;
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chem. 261:5041-5050(1986).
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                                                                                                                                                                                                                                                                                                                          Collagen;
                                       Conservative
                                                                                                                                                                                                   19
53
539
                                                                                                                                         ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMNTC1Q.
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                                                                                                                                         456
66434
                                                      6.6%;
                                                                                                                                                                                                                                                                                                                        Signal.
                                                                                                                                         WW.
                                       11;
                                                                                                                                                                                                   NONHELICAL REGION
TRIPLE-HELICAL REG
NONHELICAL REGION
C1Q.
                                                      Score 165.5; DB 1
Pred. No. 4.1e-05;
                                                                                                                                     HYDROXYLATION.
HYDROXYLATION.
EAB48B1EF174B145 CRC64;
                                                                                                                                                                                                                                                                                  COLLAGEN ALPHA 1(X) CHAIN
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rest M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Olsen B.R.; ances split the 5'-untranslated for the non-collagenous amino-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmid T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ere are no rest
as its content
                                                                          DB 1;
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                                                                                                                                                                                                                                             REGION
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                                                                                                                                                                                                                        (NC1).
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P27658;
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01-AUG-1992 (Rel. 23, 1
16-OCT-2001 (Rel. 40, 1
Collagen alpha 1(VIII)
                                                                                                                                                                                                                                                                                               InterPro; IPR001073; C1q.
InterPro; IPR000087; Collag
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COL8A1.
Homo sapiens (Human).
Homo sapiens (Human).
Chordata;
                                                                                                                                                                           Glycoprotein;
                                                                                                                                                                                                 Extracellular matrix;
                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                               PRINTS; PRODUCT; COMPLE SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                    SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WITH ALPHA 2(VIII) TYPE COLLAGENS.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT AT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDITHE HIGH THERMAL STABILITY OF THIS REGION.

SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.

SIMILARITY: CONTAINS 1 C10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                              S15435;
120251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              x57527;
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) chain precursor (Endothelial collagen).
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                    COLLAGEN ALPHA 1(VIII) CHAIN MONHELICAL REGION (NC2).
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NONHELICAL REGION (NC1).
C10.
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(VIII) chain
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89380199; PubMed-2476437; Yamaguchi N., Benya P.D., van der Rest M.,
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                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long lified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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COLLAGEN ALPHA 1(VIII)
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"Specific hybridization p
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Biochim. Biophys. Acta 11
-i- FUNCTION: TYPE X COLL
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                                                                                                                                                       Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.; "Cloning of the human and mouse type X collagen the mouse type X collagen ene to chromosome 10. Eur. J. Blochem. 206:217-224(1992).
                                                                                                                                                                                                                                                                                                               MEDLINE=93238750; PubMed=
Kong R.Y.C., Kwan K.M., I
Grant M.E., Cheah K.S.E.;
                                                                                                                                                                                                                                                                                                                                                                                               "The mouse collagen X gene: complete nucleotide structure and expression pattern."; Biochem. J. 289:247-253(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C;
MEDLINE-93143676;
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01-NOV-1995
                                                                                   Elima K., Metsaeranta M.,
                                                                                                 MEDLINE=92182017;
                                                                                                                STRAIN-C57BL;
                                                                                                                                                                                                                               STRAIN-DBA/2J;
                                                                                                                                                                                                                                                                      "Intron-exon structure, alternative use the mouse collagen X gene, Coll0a-1."; Eur. J. Biochem. 213:99-111(1993).
                                                                                                                                                                                                                                                                                                                                                         STRAIN-129/SV;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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              Acta 1130:78-80(1992)
E X COLLAGEN IS A PROD
                                                                                                   PubMed=1543751;
                                                                                                                                                                                                 PubMed=1587271;
M.F., Hayashi M
                                                                                                                                                                                                                                                                                                                             PubMed=8477738;
K.M., Lau E.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed-8424763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                              FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosati
                                                       probes
                                                                                                                             N.A.
                                                                                   Kallio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ≈.,
                                                                       В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 163.5; DB 1
Pred. No. 6.6e-05;
5; Mismatches 48
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NONHELICAL REGION (NC1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                          for
                                                                       Vuorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2A8CEF1EF8274E99 CRC64;
  LOCALIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metsaranta
                                                                                   J.,
              A PRODUCT
                                                                                                                                                                                                                                                                                                                             Thomas J.T.,
                                                        mouse
                                                                     Peraelae
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                QF
                                                                                                                                                                                                                                                                                                  promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
    PRESUMPTIVE
                                                                                   X
                HYPERTHROPHIC
                                                                                                                                                                                                                                                                                                                               Boot-Handford R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garofalo S.,
                                                          2(IX) and alpha
                                                                                                                                                                         genes
                                                                                                                                                                                                                                                                                                                                                                                                                              sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                      Eerola
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                                                                                                                                                                                    and mapping
                                                                                                                                                                                                                                                                                                   expression
                                                                                      Η.,
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                                                                                                                                                                                                                                                                                                                                                                                                                              exon
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                                                          1(X)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local
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PIR;
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EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00007; COMPLE SMART; SM00110; C10; 1. PROSITE; PS01113; C10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular matrix; Connective tissue;
                                                                                                                                            610
                                                                                                                                                                                                                           550
                                                                                                                                                                                                                                                                                                        490
                                                         664
                                                                                                  160
                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                          19 GPPAHPRP-----PEEVGPPGAPGLPQY-----TGEISEMTKCPCPDIER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L; X67348; CAA47763.1; -.
Li; X65121; CAA46237.1; -.
Li; X63013; CAA44741.1; -.
Li; Z21610; CAA79736.1; -.
L; S2807; S280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MINERALIZATION ZONES SUBUNIT: HOMOTRIMER.
                                                                                                  SSENLH 165
                                                                                                                                                                                                                                                                                                      GPPGPPGPRGHSGEPGLPGPPGPPGQAVMPDGFIKAGQRPRLSGMPLVSANHGVTGM 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:88445; CollOal.
rPro; IPR001073; C1q.
rPro; IPR000087; Collagen.
                                                                                                                                                                            CKVNIWLMRKQILANKEEISK-----QQSIQEVT----WVLLKAFSFIREAEHK---
                                                                                                                                                                                                                       PVSAFTVILSKAYPAVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHVHVKGTH
                                                         SSEYVH
                                                                                                                                      VWVGLYKNGTPTMYTYDEYSKGYLDQASGSAIMELTENDQVWLQLP
                                                                                                                                                                                                                                                           --SAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELH--H 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00386; Clq; 1.
PF01391; Collagen; 6.
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen;
                                                         669
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF HYALINE CARTILAGE
                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 159.5; DB 1 Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NONHELICAL REGION C1Q.
P -> L (IN REF. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRIPLE-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONHELICAL REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FE984CA99AF708E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              > L (IN REF. 3).
> S (IN REF. 2).
> F (IN REF. 3).
> S (IN REF. 3).
> K (IN REF. 3).
> K (IN REF. 3).
> C (IN REF. 3).
> C (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA 1(X)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REF. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                   45;
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                                                                                                                                                          Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen alpha 1(X)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00386; Clq; 1. Pfam; PF01391; Collagen; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Boyinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cartilage; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00007; COMSMART; SM00110; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S13301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 273:141-148(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collagen genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation of cDNAs encoding the complete sequence of bov collagen. Evidence for the condensed and anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen. Evidence for the condensed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Cartilage;
MEDLINE-91113131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                       69
                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF CHONDROTOCYTES AND HAS BEEN LOCALIZED TO P MINERALIZATION ZONES OF HYALINE CARTILAGE.
SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
LPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELH--HCKVNIWLMRKQI 126
                                                               AGEPGLPGPPGPPGQVALPEDFVKAGQRPFVSANQGVTGMPV----SAFTVILSKA 555
                                                                                                  AGPPAHPRPPEEVGPPGAPGLPQ------YTGEISEMTKCPCPDIERSAFTVKLSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X53556; CAA37624.1;
                                                                                                                                                        Similarity 31.8
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMNTC1Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20,
20,
38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C1Q;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain
                                                                                                                                                                                                                                                                      65546
                                                                                                                                                                          6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor.
                                                                                                                                                        16;
                                                                                                                                                                                                                                                                 NONHELICAL REGION (NC1).
C1Q.
BY SIMILARITY.
BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
N-LINKED (GLCNACC. . .) (POTENTIAL).
WW; CD4CA73A03E004CA CRC64;
                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                           NONHELICAL REGION TRIPLE-HELICAL REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NONHELICAL
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ام، 0.
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                                                                                                                                                        DB 1; I
).00013;
nes 56;
                                                                                                                                                                                                                                                                                                                                                                                                    REGION (NC1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (NC2).
                                                                                                                                                                                                  Length
                                                                                                                                                        Indels
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ID CALA_HUMAN
ID CALA_H
ID CALA_H
AC 003692
AC 003692
AC 003692
AC 003692
AC 001090
DT 01-NOV
DT 16-OCT
COLLA9
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Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, II)
associated collagen (type IX), and network-forming
cause a spectrum of diseases of bone, cartilage, ar
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                                                                                                                                                                                                                                                                                                                  Apte S., "Cloning
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Submitted
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91243838;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Apte S.S., Seldin M.F., Hayashi M., Commonsory of the human and mouse type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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Mammalia; Eutheria;
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"Novel missense mutation resulting in the subs
cysteine at codon 597 of the type x collagen g
Schmid metaphyseal chondrodysplasia.";
J. Hum. Genet. 43:259-261(1998).
i- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF
CHONDROTOCYTES AND HAS BEEN LOCALIZED TO P
MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                      wakiants SMCD GLU-18 AND ARG-18;
MEDLINE-97220591; PubMed-9067753;
Ikegawa S., Nakamura K., Nagano A
"Mutations in the N-terminal globu
gene (COL10Al) in patients with so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96375754; PubMed-8782043; Wallis G.A., Rash B., Sykes B., Bonaventure J., Maroteaux P., Wallis G.A., Rash B., Sykes B., Bonaventure J., Maroteaux P., Zabel B., Wynne-Davies R., Grant M.E., Boot-Handford R.P.; "Mutations within the gene encoding the alpha 1 (X) chain of type collagen (CCIOA1) cause metaphyseal chondrodysplasia type Schmid not several other forms of metaphyseal chondrodysplasia."; J. Med. Genet. 33:450-457(1996).
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"Type X collagen multimer assembly in vitro is prevented to Val mutation in the alpha 1(X) NC1 domain resulting in metaphyseal chondrodysplasia.";
J. Biol. Chem. 270:4558-4562(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grant M.E., Boot-Handford R.P.;
"Amino acid substitutions of conserved residues i carboxyl-terminal domain of the alpha 1(X) chain occur in two unrelated families with metaphyseal
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Bonaventure J., Chaminade F., Maroteaux
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MEDLINE=99069781; PubMed=9852679;
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Am. J. Hum. Genet.
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"Mutations in three subdomains
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MEDLINE=95181449; PubMed=7876225;
Chan D., Cole W.G., Rogers J.G.,
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VARIANTS SMCD ASP-598 AND
MEDLINE-94136476; PubMed-8
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MEDLINE=94272470; Pub
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CHONDROTOCIAL CONES OF HYALING CONTRINER.
MINERALIZATION ZONES OF HYALING CONTRINER.
SUBUNIT: HOMOTRIMER.
PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
PTM: PROLINES AT THE THIRD POSITION OF THE CHAINS.
PTM: G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
PTM: CG-X-Y) ARE THE CAUSE OF SCHMID TYPE
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63:1659-1662(1998).
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R; S43901; A43901.

R; S18249; S18249.

R; S21856; S21856.

R; S26396; S26396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; X60382; CAA42933.1; -. X60382; CAA46236.1; -. X85120; CAA46236.1; -. X89568; CAA67178.1; -. X68531; AAC60615.1; -. X58531; AAC60615.1; -. X5879; CAA41686.1; -. X5879; CAA41679; CAA51170.1; -. X672579; CAA51170.1; -. X60579; CAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: DEFECTS IN COL10A1 ARE THE CAUSE OF SPONDYLOMETAPHYSEAL DYSPLASIA (SMD). SMD COMPRISES A HETEROGENEOUS GROUP OF HERITABLE SKELETAL DYSPLASIAS CHARACTERIZED BY MODIFICATIONS OF THE VERTEBRAL BODIES OF THE SPINE AND METAPHYSES OF THE TUBULAR BONES SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a capen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METARHYSEAL CHONDRODYSPLASIA (SMCD), A DOMINANTLY INHERITED DISORDER OF THE OSSEOUS SKELETON: THE CARDINAL FEATURES OF THE DISORDER ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GAIT. RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, FLARING OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAPHYSES, AND A WIDE IRREGULAR GROWTH PLATE,
KLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELHHCK-VNIWL 121
                                        SGEPGLPGPPGPPGQAVMPEGFIKAGQRPSLSGTPLVSANQGVTGMPVSAFTVILSK
                                                                                  AGPPAHPRPPEEVGPPGAPGLPQ---YTGEISEMTKCPCPDIER-----SAFTVKLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00386; C1q; 1.
PF01391; Collagen; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spr00007; COMPLE
sm00110; C1Q; 1.
E; PS01113; C1Q;
                                                                                                                                 39;
                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collagen;
                                                                                                                                                                                                                                                                                                                                                                                            19
19
57
520
545
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMNTC1Q
                                                                                                                                                                                                                                                                                                                                                                                            18
56
519
680
680
                                                                                                                                                                                                                                                               591
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                                                                                                                                                   6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal;
                                                                                                                               16;
                                                                                                                                                 Score 156; DB 1;
Pred. No. 0.00022;
                                                                                                                                                                                                                                                                                                                                               G -> E (IN SMCD).
/FTId=VAR_001838.
G -> R (IN SMCD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
COLLAGEN ALPHA 1(X) CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disease mutation;
                                                                                                                                                                                                                                        C -> R (IN SMCD).
/FTId=VAR_001841.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NONHELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRIPLE-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NONHELICAL
                                                                                                                                                                                                                                                                                     /FTId=VAR_001840.
                                                                                                                                                                                                                                                                                                                             /FTId=VAR_001839
                                                                                                                                                                                                                                                                                                            v
                                                                                                                                                                                                                    v
                                                                                                                               Mismatches
                                                                                                                                                                                                                  E (IN SMCD AND SMD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                       REGION
                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NC2).
                                                                                                                                                                       Length
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESPECIALLY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γď
                                                                                                                                                                          680;
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                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            commercial
                                                                                  67
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Db 561 AYPAIGTDIPFDKILYNRQQHYDPRTGIFTCQIPGIYYFSYHV---HVKGTHVWV 612
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APM1_MOUSE
                                                                                                                                                                                                                          RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Salto R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl R., Chaubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L., M., Staubli F., Suzuki R., Tomita M., Wagner L.,
Ras Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D. A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Rayashiraki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     060994; Q62400; Q9DC68; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Adiportin precursor (30 kDa adipocyte complement-related (ACRP30) (Adipocyte specific protein Adipoc).

APM1 OR ACRP30 OR ADIPOQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Chromosomal localization, expression pattern, and promoter analysis of the mouse gene encoding adipocyte-specific secretory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11162643;
Das K., Lin Y., Widen E.,
"Chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Adipocyte;
MEDLINE-96070757; PubMed-7592907;
Scherer P.E., Williams S., Foglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                     Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A novel serum protein adipocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APM1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                    Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hu E., Liang P., Spiegelman B.M.;
"AdipoQ is a novel adipose-specific gene dysregulated in obesity.";
J. Biol. Chem. 271:10697-10703(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96209999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                          Functional annotation of a full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLANMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES (BY SIMILARITY). SUBUNIT: HOMOOLIGOMER. SUBUNIT: HOMOOLIGOMER. SUBCELLULAR LOCATION: SECRETED IN PLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270:26746-26749(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8631877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S., Fogliano M., similar to Clq, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Commun. 280:1120-1129(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshino M., Itoh M., Isnii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scherer P.E.;
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produced
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exclusively
                                                                                                                                                                                          collection.";
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Best Local Similarity
Matches 44; Conser
                     Q15848;
01-NOV-1997
01-NOV-1997
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
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SEQUENCE
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DISULFID
MOD_RES
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                                                                                                                   HUMAN
                                                                                               APM1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SMUULLY, TOIQ; 1. PROSITE; PS01113; C1Q; 1. Collagen; Signal; Repeat; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00386; Clq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                          208
                                                                                                                                                                                                                              149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECRETED INTO SERUM.
INDUCTION: DURING HORMONE-INDUCED
ACTIVATED BY INSULIN.
                                                                                                                                                                                        LEVGDQVWLQVYGDGDH---NGLYADNV
                                                                                                                                                                                                                          A----FSFIREAEHKSSENLHPDNV
                                                                                                                                                                                                                                                               GSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLH
                                                                                                                                                                                                                                                                                                 EAMGVFACRVPGNYYSSFDVELH--HCKVNIWLMRKQILANKEEISKQQSIQEVTWVLLK 148
                                                                                                                                                                                                                                                                                                                                                                          GPPGAPGLPQYTGEISEMTKCPCPDIERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:106675; Acrp30.
rPro; IPR001073; C1q
                                                                                                                                                                                                                                                                                                                                      GPRGFPGTPGRKGEPGEAAY-----MYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U37222; AAA80543.1; -. U49915; AAB06706.1; -. AF304466; AAK13417.1; -. AK003138; BAB22597.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; PR00007; COM
SM00110; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000087; Collagen.
                     (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA:
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMNTC1Q.
                     35,
41,
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47
50
56
56
79
107
113
113
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26841 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%;
29.7%;
Last sequence update)
Last annotation update)
(30 kDa adipocyte complement-related
                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydroxylation; Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (BY
HYDROXYLATION (I
HYDROXYL
                                                                                                                                                                                                                                                                                                                                                                                                             Score 152.5; DB 1
Pred. No. 0.00012;
3; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLLAGEN-LIKE C1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADIPONECTIN
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137B687D873988C4 CRC64;
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                                                                                                                                                                                                                            169
                                                                                             244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADIPOSE DIFFERENTIATION
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(BY SIMILARITY).
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   protein)
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MEDLINE-20440368; PubMed-10982546; Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohr Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y. "Adiponectin, an adipocyte-derived plasma protein, ir endothelial NF-kappaB signaling through a CAMP-depend Circulation 102:1296-1301(2000).
                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the E
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
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"The human apM-1, an adipocyte-specific gene linked to the family of TNF's and to genes expressed in activated T cells, is mapped to chromosome 1921.3-923, a susceptibility locus identified for familial combined hyperlipidemia (FCH).";
Biochem. Biophys. Res. Commun. 260:416-425(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               negatively regulates the growth functions of macrophages."; Blood 96:1723-1732(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDLINE=20417747; PubMed=10961870;
Yokota T., Oritani K., Takahashi I.,
Ouchi N., Kihara S., Funahashi T., To
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[3]
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MEDLINE-96224171; PubMed-8619847;
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Mammalia; Eutheria;
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APM1 OR ACRP30 OR GBP28.
                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsuzawa Y.;
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Biochem. Biophys. Res. Commun. 221:286-289(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: EXPRESSED ONLY IN THE SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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SUBCELLULAR LOCATION: SECRETED IN PLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: INFORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF SUPPRESSION OF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES
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D45371; BAA08227.1;
AB012165; BAA86716.:
AB012164; BAA86716.:
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                                                                                                                                                                        email to license@isb-sib.ch).
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Tenner A.J., Tomiyama Y.,
                                                                                                                                                                                                           moved. Usage by and for (See http://www.isb-sib.
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cAMP-dependent
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Mammalia; Eutheria;
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Collagen; Signal; Repeat; Hydroxylation;
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Pfam; PF01391; Collagen;
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InterPro; IPR000087; Coll
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VIII) chain (Endothelial collagen) (Fragment).
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COLLAGEN-LIKE.
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                                                                                                                                           Hominidae;
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AND
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                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                            244;
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RESULT 14
C1QC_HUMAN
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Best Local :
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P02747;
21-JUL-1986 (Rel. 01, 0
01-JUL-1993 (Rel. 26, 1
16-OCT-2001 (Rel. 40, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial contents are removed to the statement of the statement is not removed.
                                                                                         Sellar G.C., Blake D.J., Reid K.B.M.; "Characterization and organization of the genes encoding the A-, and C-chains of human complement subcomponent Clq. The complete derived amino acid sequence of human Clq.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 7.
SMART; SM00110; ClQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Complete amino acid sequences
present in subcomponent Clq of
                          MEDLINE=80020137;
Reid K.B.M.;
                                                                                                                                          TISSUE=Monocytes;
MEDLINE=91174759; PubMed=1706597;
                                                                                                                                                                                            Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                Complement Ciq subcomponent, C chain precursor, C1QG OR C1QC.
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                                                      SEQUENCE OF
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular matrix; Connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01113; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                            559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 GPPGVPGSPGITGPPGLPGPPGAPGAFDETGIAGLHLPNGGVEGAVLGKGGKPQFGLGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                             502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 GPPAHPRPPEEVGPPGAPGLPQYTGEISEM----TKCPCPDIERS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 C10 DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                   HCK-VNIWL
                                                                                                                                                                                                                                                                                                                                                                                                                                            SAHATPAFTAVLTSPLPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAYHV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000087;
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12
469
500
635 /
                           29-122.
20137; PubMed=486087;
                                                                              274:481-490(1991).
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                                                                                                                                                                                                                                                                                                                             STANDARD;
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468
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Last annotation updat
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TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
C1Q.
C1Q.
W; 22A261164754F771 CRC64;
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Pred. No. 0.(
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Catarrhini;
  of the thi
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                                                                                                                                                                                                                                                                                                                             245
              three collagen-like
                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
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   component
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                                                                                                                                                                                                            Hominidae;
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              regions
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Biochem.
[3]
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VARIANT
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DISULFID
MOD_RES
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1- PTM: O-LINKED GLYCANS CONSIST OF GLG-GAL DISACCHARIDES.

1- DISEASE: DEFECTS IN CLOG ARE A CAUSE OF CLO DEFICIENCY. IT IS RARE GENETIC DISORDER WHICH IS ASSOCIATED WITH RECURRENT INFECTIONS AND A HIGH PREVALENCE OF LUPUS ERYTHEMATOSUS-LIKE SYMPTOMS. IT IS CHARACTERIZED BY A LOSS OF ACTIVATION OF THE COMPLEMENT CLASSICAL PAPHWAY.

1- SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00007; COMPLE SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00386; Clq; 1. Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001073; Clq. InterPro; IPR000087; Coll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunobiology 199:286-294(1998).
-I- FUNCTION: C1Q ASSOCIATES WITH THE PROCE.
C1, THE FIRST COMPONENT OF THE SERUM
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                     Complement
                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98450587; PubMed=9777412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVIEW OF C10 DEFICIENCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular basis of hereditary Clq deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT C1R(2)C1S(2) PROGNEZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES. SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lement.";
nem. J. 179:367-371(1979).
                                                                                                                                                                                                                                                                                                                                                                                         Signal;
                                                                                                                                                                                                                                                                                                                                                                                                    PSO1113; C1Q; 1.
nt pathway; Plasma;
  57
66
72
84
87
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S14351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C1HUQC
                                                                                                                                                                                                                                                                                                                                                                                         Disease mutation.
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57
66
72
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87
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25748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collagen
   HYDROXYLATION.

G -> R (IN C10 DEFICIENCY).

/FTId-VAR 008542.

K -> P (IN REF. 2).

P -> K (IN REF. 2).

K -> P (IN REF. 2).

N -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                   Hydroxylation; Glycoprotein;
                                                                                                                                                           O-LINKED (GAL.
                                                                                                                                                                                              O-LINKED (GAL.
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 -> D (IN REF. 2)
-> N (IN REF. 2)
EF184EDB4DF45DB8
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COMPLEMENT SYSTEM.
                                                                                                                                                                                                                                                                                                                                                               SUBCOMPONENT, C CHAIN
                                                                                                                                                                                                                                                                                                                               OTHER
                                                                                                                                                                                                                                                                                                                             C CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                 Collagen;
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Best Local S
Matches 39
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DOMAIN
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF095154; AAC64186.1; -. InterPro; IPR001073; C1q. InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed in areas of the brain involved in mot Brain Res. Mol. Brain Res. 63:233-240(1999).
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=99097006; PubMed=9878755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00007; COMPLE SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berube N.G., Swanson
Baskin D.S., Smith J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clq-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berube N.G., Swanson X.H., Bertram M.J. Baskin D.S., Smith J.R., Pereira-Smith Baskin of CRF, a "Cloning and characterization of CRF, a
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
    137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 APNSLIRFNAVLTNPQGDYDTSTGKFTCKVPGLYYFVYHAS-HTANLCVLLYRSGV 187
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KNPHEGYEVLKFDDVVTNLGNNYDAASGKFTCNIPGTYFFTYHV
                                                                                                                                   GPPAHPRPPEEVGP-----
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                                          KLPLP-FKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDV
                                                                                        GPPGDPGPPGPVGPPGEKGEPGKPGPPGLPGAGGSGAISTATYTTVP---
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                                                                                                                                                                                  l Similarity
37; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01113;
                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
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17
67
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258
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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115
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35.6%;
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                                                                                                                                                                                  10;
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C1Q-RELATED FACTOR.
COLLAGEN-LIKE.
C1Q.
%W; 52C51CDF59CAEZBF CRC64;
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                                                                                                                -PGAPGLPQY--TGEISEMTKCPCPDIERSAFTVKLSG 67
                                                                                                                                                                                Score 124.5;
Pred. No. 0.01
[0; Mismatches
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a novel Clq-related factor,
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Search completed: June 30, 2002, 11:54:49 Job time: 145 sec

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Title:
Perfect score:
                                                                                            Run
                                                                                                                               OM protein - protein search, using sw model
   US-09-997-610-2
2494
                                                                                            June 30,
                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                    2002, 11:51:29 ; Search time 20.93 Seconds (without alignments) 2107.263 Million cell updates/sec
                                                                                                                                                                                     Compugen Ltd
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Sequence: IVVIPVLITAVIEHVEVAGP...........GQFFPFGTAVFTQCLYLHCM 459

Scoring table: Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s PIR_71:* summaries

Database

4321 pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10		8	7	6	ر د	4	ω	N	_	Result No.
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4.0	4.0	4.1	4.1	4.1	4.2	4.3	4.4	4.4	4.4	4.4	4.5	4.7	4.9	5.2	•	5.9			6.4			6.6		6.7		6.9	٠	13.2	Query Match I
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hypothetical prote	lement Clq	GZF3 protein - yea	DNA repair protein	homeotic protein H	complement subcomp	phosphatidic acid-	cell-cycle-depende	vsaA protein precu	complement subcomp	_			hypothetical prote	rab3 effector prot	complement subcomp	2	<u>.</u> .	_		alpha 1	alpha 1	alpha 1	alpha 1	collagen alpha 1(V	hibernation-relate	collagen alpha 1(V	hibernation-relate	hibernation-relate	Description

ALIGNMENTS

hibernation-related protein HP-20 precursor - Siberian chipmunk (;Species: Eutamias sibiricus (Siberian chipmunk) C;Species: Eutamias sibiricus (Siberian chipmunk) C;Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: A48150; C41752 R;Takamatsu, N.; Ohba, K.; Kondo, J.; Kondo, N.; Shiba, T. Mol. Cell. Biol. 13, 1516-1521, 193
A;Title: Hibernation-associated gene regulation of plasma proteins with a collagen-li A;Reference number: A48150; MUID:93180798

A; Molecule type: mRNA; protein A; Residues: 1-196 < TAK>

A;Cross-references: GB:D12974; NID:g287467; PIDN:BAA02351.1; PID:g287468
A;Note: the source is designated as Tamias asiatious in Genbank entry TMSHP20A, relea
A;Note: sequence extracted from NCBI backbone (NCBIN:125943, NCBIP:125944)
R;Kondo, N.; Kondo, J.
R;Kondo, N.; Kondo, J.
R;Bill. Chem. 267, 473-478, 1992

J. Biol. Chem. 267, 473-478, 1992 A;Title: Identification of novel blood proteins specific for mammalian hibernation. A;Reference number: A41752; MUID:92112696 A;Accession: C41752

A;Status: preliminary
A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Mesidues: 24-58;66-99;104-129;132-136;137,151-184 <KON>
A;Residues: 24-58;66-99;104-129;132-136;137,151-184 <KON>
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal C;Keywords: glycoprotein; hibernation; plasma
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-196/Product: hibernation-related protein HP-20 #status experimental <MAT>
F;73-196/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;154/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Best Local S Matches 69 Similarity Conservative 13.2%; Score 330; DB 2; 146.9%; Pred. No. 1.6e-18; ative 21; Mismatches 45; Length 196; Indels 12; Gaps

4.

ρ 1 IVVIPVLITAVIEHVEVAGPP----AHPRPPEEVGP------PGAPGLPQYTGEISEMTKC 51

В 7 LAIFVLMVNVLNDQVSCSGPPGPVGYPGVPGVPGPRGPPGQPGAAGRPGDPGPKGPSVKC 66

Ş 52 PCPDIERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVE 111

PCR--ERSAFTVKFSGRLPPPSEPVVFTEVLYNTQRDLKESTGVFNCVEPGNYHFSFDVE 124

112 LHHCKVNIWLMRKQI-LANKEEISKQQ 137

В

67

밁 125 LYHCKVKIGLMKNHIQVMEKHQLSKNE 151

RESULT B48150 N

hibernation-related protein HP-25 precursor -Siberian chipmunk

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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 29-62;84-130;172-183;187-192;201-215 <KON>
C;Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom C;Keywords: glycoprotein; hibernation; plasma
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-215/Product: hibernation-related protein HP-25 #status experimental <MAT>
F;91-214/Domain: complement C1q carboxyl-terminal homology <C1Q>
F;167/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C:Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: B48150; B41752
R;Takamatsu, N.; Obba, K.; Kondo, J.; Kondo, N.; Shiba, T.
Mol. Cell. Biol. 13, 1516-1521, 1993
A;Title: Hibernation-associated gene regulation of plasma proteins with a cc A;Reference number: A48150; MUID:93180798
                                                                                                                                                                                                                             A;Cross-references: EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g1359953 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology F;616-742/Domain: complement C1q carboxyl-terminal homology <C1Q>
                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Biochem. 207, 895-902, 1992
A;Title: Alpha-1(VIII)-collagen gene transcripts encode a
A·Poference number: S23779; MUID:92362626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collagen alpha 1(VIII) chain - mouse C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession:
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J. Blol. Chem. 267, 473-478, 1992
A;Title: Identification of novel blood proteins specific A;Reference number: A41752; MUID:92112696
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-743 < MUR>
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA; protein A; Residues: 1-215 <TAK>
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                                                   GPPAHPRPPEEVGPPGAPGL---PQYTGE-ISEM-----TKCP-----CPDIE 57
GQPGLPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGVKTPHAYAGKKGKHGGPAYE 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLSERPPEPFQPIVFKEALYNQEGHFNMATGEFSCVLPGVYNFGFDIRLFQSSVKIRLMR
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                                                                                                                                 6.9%;
27.4%;
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                                                                                              Score 171; up ...
pred. No. 2.4e-05;
                                                                                                         26;
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Pred. No. 6.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-Sep-1999 #text_change 16-Jun-2000
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                                                                                                                                                       Length 743;
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hibernation-related protein HP-27 precursor - Siberian chipmunk
C;Species: Eutamias sibiricus (Siberian chipmunk)
C;Date: 16-Feb-1994 **sequence_revision 25-Apr-1997 **text_change 20-Jun-2000
C;Accession: C48150; A41752
R;Takamatsu, N.; Obba, K.; Kondo, J.; Kondo, N.; Shiba, T.
Mol. Cell. Biol. 13, 1516-1521, 1993
A;Title: Hibernation-associated gene regulation of plasma proteins with a collagen-li
A;Reference number: A48150; MUID:93180798
A;Accession: C48150
A;Molecule type: mRNA; protein
A;Residues: 1-215 <TAK>
A;Noteule type: mRNA; protein
A;Residues: 1-215 <TAK>
A;Note: the source is designated as Tamias asiaticus in Genbank entry TMSHP27, releas
A;Note: the source is designated from NCBI backbone (NCBIN:125948, NCBIP:125949)
R;Kondo, N.; Kondo, J.
J. Biol. Chem. 267, 473-478, 1992
A;Title: Identification of novel blood proteins specific for mammalian hibernation.
A;Reference number: A41752; MUID:92112696
                                                                                                                                        collagen alpha l(VIII) chain - chicken C;SpecLes: Gallus gallus (chicken) C;Date: 10-Sep-1999 #sequence_revision C;Accession: S23298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: complement Subcomponent Clq chain A; complement Clq carbox C;Keywords: glycoprotein; hibernation; plasma C;FoyDomain: signal sequence #status predicted <SIG> F;31-3U5/Product: hibernation-related protein HP-27 #status experimental F;91-214/Domain: complement Clq carboxyl-terminal homology <ClQ> F;155/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C48150
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., A; Title: The molecular biology of collagens with short triple-he A; Reference number: $22243
                                                                                    R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; maguchi, N.; Olsen, B.R.
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A; Residues: 31-40,'A',42-50,'Q',52-215 <KON>
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Best Local
                                                                                                                                                                                                                                                                                                                                                                        133 GLYQFGFHIEAVQRAVKVSLMRNGTQVMEREAEAQDGYEHIS
                                                                                                                                                                                                                                                                                                                                                                                                                            102 GNYYSSFDVELHHCKVNIWLMRKQILANKEEISKQQSIQEVT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           716 QNPFEQ 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 KNPFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    671 GNVWVALFKNNEPMMYTYDEYKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 VNIWLM----RKQILANKEEISKQQSIQEVTWVLLKAFSFIREAEHKSSENLHPDNVIKK 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VLITAVIEHV------EVAGP------PAHPRPPEEVGPPGAPGLPQY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILALSVLMHVVCSETQGNPESCNVPGPQGPPGMRGPPGTPGKPGPPGWNGFPGLPGPPGP 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGEISEMTKCPCPDIERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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31.5%;
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Pred. No. 9.4e-06;
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                                                                                                                                                                     10-Sep-1999 #text_change 10-Sep-1999
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                             triple-helical
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                                                                                                                 Jacenko,
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                                                       pp.79-114, Academic
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                                                                                                              O.; LuValle,
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A; Accession: S23298
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-744 <NII
                                                                                                                                                                                                           A:Molecule type: DNA A:Molecule type: DNA A:Residues: 'T',9,'D',11-12,'EDQMKLYILFTM',30-31,'TCKSGRAFTTYMILQNVMADLVSSHT',629,'PQAVLSLISMFTIKCGSSCQIQNPMVSIPLNMFILLSQVSYLLKSNNIPLTMS' <NIN1>A;Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700 A;Accession: S77711
                                                                                                              A; Molecule type: protein
A; Residues: 104-112, 'X', 114-117; 453-466 <NIN2>
C; Superfamily: collagen alpha 1(VIII) chain; complement
C; Keywords: coiled coil; extracellular matrix; glycoprot
                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-75 < LUV-
R; Ninomiya, Y.; Gordon, M.; van der Rest, M.
T; Biol. Chem. 261, 5041-5050, 1986
A; Title: The developmentally regulated type
A; Reference number: 150218; MUID:86168227
A; Accession: S65594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; J. Biol. Chem. 263, 18378-18385, 1988 A;Title: The type X collagen gene. Intron sequestable and the collagen gene and the collagen gene. A;Reference number: A31896; MUID:89054019 A;Accession: A31896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Gallus gallus (chicken)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S23297; A31896; S65594; S77711; I50218
R;Ninomiya, Y: Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, maguchi, N.; Olsen, B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-674 <NIN>
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                                                                       F;547-673/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Reference number: S22243
A:Accession: S23297
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in Extracellular Matrix Genes, A; Title: The molecular biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(X) chain precursor -
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, reywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline; ;1-18/Domain: signal sequence #status predicted <SIG>;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>;453,456/Modified site: hydroxyproline (Pro) #status experimental; ;611/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMPAFTAELTAPFPPVGAPIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYFAYHV---HCK 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELHHCK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQPGLPGPPGPPGPPAVMPPTPAPQGEYLPDMGLGIDGVKTPHAYAAKKGKNGGPAY 613
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C1q carboxyl-terminal homology <C1Q>
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Pred. No. 5.5e-05;
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Query Match

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Score 165.5;

DB

<u>ب</u>

Length

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A; Title: The complete primary structure o A; Reference number: S15435; MUID:91231001
                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(VIII) chain precursor - human
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
S15435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:J05042; NID:g164895; PIDN:AAA31204.1; C;Superfamily: collagen alpha 1(VIII) chain; complement C1q (F;1-20/Domain: signal sequence #status predicted cSIGs F;21-744/Product: collagen alpha 1(VIII) chain #status predicted collagen alpha 1(VIIII) chain #status predicted c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 264, 16022-16029, 1989 A; Title: The cloning and sequencing of alphal(VIII) collagen omains similar to those of type X collagen.
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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A;Cross-references:
C;Genetics:
                                                          A; Molecule type: mRNA
A; Residues: 1-744 < MUR>
                                                                                                                                                                                                                                              Eur. J. Biochem. 197, 615-622,
                                                                                                                                                                                                                                                                        C; Accession: S15435
R; Muragaki, Y.; Mattei, M.G.; Yamaguchi,
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A; Residues: 1-744 < YAM>
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R; Yamaguchi, N.; Ber
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                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPAHPRPPEEVGPPGAPGL----PQYTGE-ISEM-----TKCP-----CPDI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVILSKAYPGATVPIKFDKILYNRQQHYDPRTGIFTCRIPGLYYFSYHV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGPPAHPRPPEEVGPPGAPGLPQ--YTGEISE------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGEPGLPGPPGPPGQSTIPEGYVKGESRELSGMSFMKAGANQALTGMPV----SAF 548
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                             EMBL: X57527; NID: g30081; PIDN: CAA40748.1;
                                                                                                                                                                                                                                                                                                                                         #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
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Pred. No. 9.4e
l6; Mismatches
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l; Mismatches
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                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                              N.; Olsen,
                                                                                                                                                                                                                    the
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                                                                                                                                                                                                                    alpha-1(VIII)
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                             PID: 930082
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A;Title: The mouse collagen X gene: complete nucleotide sequence, exon st A;Reference number: $28807; MUID:93143676
A;Moleowile 1.
                                        A;Molecule type: mRNA, A;Molecule type: mRNA, A;Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'A;Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'A;Repte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R. Eur. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S31216; S28807; S22211; S30127; I48299; S26397; S31830
R:Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; G:
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F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F;21-117/Region: amino-terminal nonhelical
F;118-571/Region: interrunted half--'
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A;Cross-references: GDB:128104; OMIM:120251
A;Map position: 3q11.1-3q13.2
C;Superfamily: collagen alpha 1(VIII) chain
F;1-20/Domain: signal sequence #status pred
  A; Reference number:
A; Accession: I48299
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R;Kong, R.Y.C.; Kwan, K.M.; Lau, E
Eur. J. Biochem. 213, 99-111, 1993
                                                                                                                                                                                                           A; Title: Characterization of the mouse type X collagen gene A; Reference number: S30127; MUID:93261348
A; Accession: S30127
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRN A;Reference number: S22215; MUID:92182017
A;Accession: S22215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; P:R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, Biochim. Biophys. Acta 1130, 78-80, 1992
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                                                                                                                                                                                                                                                                                      R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 385-450, 'K', 452-627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-285, 'A', 287-680 <ELI>
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                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID:g49796
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQPGLPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHATG--AKKGKNGGP 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lpha 1(X) chain precursor - mouse
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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                          I48299; MUID:92267014
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30.0%;
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                                                                                                                                                                                                                                                                                                                                                                    <ELA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
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Pred. No. 9.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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a, I.; Garofalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
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Matches

Conservative

16;

Mismatches

Indels

16;

Gaps

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18

AGPPAHPRPPEEVGPPGAPGLPQ-----YTGEISEMTKCPCPDIERSAFTVKLSGK 68

AGEPGLPGPPGPPGPPGQVALPEDFVKAGQRPFVSANQGVTGMPV----SAFTVILSKA 555

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RESULT
S13301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolog (;Keywords: colled coll; extracellular matrix; glycoprotein; homotrimer F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT> F;553-679/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Summers, T.A.; Irwin, M.H.; Mayne, Ř.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using A;Reference number: S26397; MUID:88087150
A;Accession: S26397
A;Molecule type: protein
A;Residues: 'SDGYFSQ',24-26,'KQ' <SUM>
                                                                                            F;1-\bar{1}8/Domain: signal sequence #status predicted \langle SI\bar{G} \rangle F;19-674/Product: collagen alpha 1(X) chain #status predicted <MAT> F;547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>
                                                                                                                                                                                                                                                                                                                                            Biochem. J. 273, 141-148, 1991
A; Title: Isolation of cDNAs encoding the A; Reference number: S13301; MUID:91113131
A; Accession: S13301
                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen alpha 1(X) chain precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 21-Nov-193 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999 C;Accession: S13301 R;Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: Coll0a-1
A;Map position: 10
A;Introns: 51/3
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A;Molecule type: DNA
A;Residues: 52-247, 'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C'
A;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
                                                                                                                                                                  C; Superfamily: collagen alpha 1(VIII) chain; concerns collection; extracellular matrix;
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                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264
                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-674 <THO>
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                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 SSENLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 VWVGLYKNGTPTMYTYDEYSKGYLDQASGSAIMELTENDQVWLQLP-----NAESNGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 CKVNIWLMRKQILANKEEISK-----QOSIQEVT-----WVLLKAFSFIREAEHK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550 PVSAFTVILSKAYPAVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHVHVKGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 --SAFTYKLSGKLPLPFKPIIFTGYLYNAQRDLKEAMGYFACRYPGNYYSSFDYELH--H 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GPPAHPRP-----PEEVGPPGAPGLPQY-----TGEISEMTKCPCPDIER-----
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  Similarity
                                                                                                                                                                                                 collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolog
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6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
Score 159; DB 2; Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 159.5;
Pred. No. 0.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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0.00017;
nes 68;
                                                                                                                                                                          glycoprotein; homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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A; Notecule type: DNA
A; Molecule type: DNA
A; Residues: 'TIPFYGWVCWVCLL', 52-680 <APT>
A; Cross-references: EMBL: X65120; NID: 923129
A; Note: the initial difference is probably due
A; Note: the initial difference B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 561-647, 'G', 549-666 <AP2>
A; Residues: 561-647, 'G', 549-666 <AP2>
A; Cross-references: EMBL: X58879; NID: g30013; PIDN: CAA41686.1; PID: g30014
R; Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, Biochem. J. 280, 617-623, 1991
A; Title: The human collagen X gene. Complete primary translated sequence and A; Reference number: S18249; MUID: 92109659
A; Accession: S18249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Apte, S.; Mattel, M.G.; Olsen, B.R.
FBBS Lett. 282, 393-396, 1991
A;Title: Cloning of human alpha-1(X) collagen
A;Reference number: S15826; MUID:91243838
A;Accession: S15826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
C;Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
R;Reichenberger, E; Beier, F; LuValle, P; Olsen, B.R.; von der Mark, K.;
          eg Ç
                                                                                                   A;Molecule type: mRNA
A;Residues: 520-597,'D',599-680 <WAL>
A;Cross-references: GB:S68531; NID:9545180; PIDN:AAC60615.1; PID:g545181
                                                                                                                                                                                                          A; Reference number: A; Accession: I51870
                                                                                                                                                                                                                                                                                      Am. J. Hum. Genet. A; Title: Amino aci
                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796 A;NOte: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014) R;Wall1s, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, Am. J. Hum. Genet. 54, 169-178, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: In situ hybridization studies on the expression of type X collagen A;Reference number: A43901; MUID:92077285 A;Accession: A43901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Reichenberger, E.; Aigner,
Dev. Biol. 148, 562-572, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
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CGHU1D
Collagen alpha 1(X) chain
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                                                         A; Note:
                                                                                 A; Note:
                                                                                                                                                                                  A; Status: translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                            pe Schmid.
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A; Residues: 547-656 < RE2>
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A; Residues: 1-26, 'T', 28-680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data A; Reference number: S30085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-680 <REI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; GB:S47714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate
                               Comment: Prolines
          and
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  mutant sequence from patient with metaphyseal chondrodysplasia a second mutant sequence with 614-Pro is also described nt: Prolines and lysines at the third position of the tripeptide subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                      Amino acid substitutions
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                                                                                                                                                                                                                                    MUID: 94136476
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Query Match
Best Local S
Matches 43
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A; Mosecular A; Residues: 19-38; ys-100; A; Residues: 19-38; ys-100; C; Comment: This protein is an endogenous:
C; Comment: This protein is an endogenous:
C; Genetics:
A; Gene: apM1
C; Superfamily: unassigned collagens; complement Clq carboxyl-terminal home C; Keywords: adipose tissue; glycoprotein; hydroxyproline
F; 1-18/Domain: signal sequence #status predicted <SIG>F; 1-18/Domain: signal sequence #status predicted <SIG>F; 19-244/Product: gelatin-binding 28kDa protein #status experimental <MAT F; 42-107/Region: collagen-like
F; 114-241/Domain: complement Clq carboxyl-terminal homology <ClQ>F; 95/Modified site: 4-hydroxyproline (Pro) #status experimental
F; 230/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: JC4700, JCARCOMMUNICA, I.; runa,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: GDB:COL10A1
A;Cross-references: GDB:128
A;Map position: 6q21-6q22
A;Introns: 52/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gelatin-binding 28K protein precursor - human
N;Alternate names: adipose specific collagen-like factor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change
C;Accession: JC4708; JC4944
R;Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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F:520-680/Domain: amino-terminal nonhelical #status predicted <NCl>
F:552-679/Domain: complement Clg carboxyl-terminal homology <ClO>
F:617/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: collagen alpha 1(VIII) chain; complement C;Keywords: colled col; extracellular matrix; glycopro F;1-18/Domain: signal sequence #status predicted <SGS F;19-680/Product: collagen alpha 1(X) chain #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: a defect in this gene may C; Complex: type X collagen may be C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
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Best Local S
Matches 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELHHCK-VNIWL 121
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33.9%;
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a homotrimer
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Pred. No. 0.00032;
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phomotrimer; hydroxylysin
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R;Sellar, G.C.; Blake, D.J.; Reid, K.B.M.
Blochem. J. 274, 481-490, 1991
A;Title: Characterization and organization of A;Reference number: $14350; MUID:91174759
A;Accession: $14351
A;Status: not compared with conceptual transl.
A;Molecule type: DNA
A;Residues: 1-245 <SEL>
**R;Reid, K.B.M.
                                                                                                                                                                                      complement subcomponent C1q chain C precursor - human k;Alternate names: complement subcomponent C1q gamma chain C;Species: Homo sapiens (man) C;Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change C;Accession: S14351; A03207
                                                                                                                                                                                                                                                                                                  RESULT
C1HUQC
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C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carbo E;1-11/Domain: amino-terminal nonhelical (fragment) #status predi E;12-468/Region: interrupted helical E;12-468/Region: interrupted helical #status predicted E;469-635/Domain: carboxyl-terminal nonhelical #status predicted E;508-634/Domain: complement Clq carboxyl-terminal homology <Clp>
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A; Residues: 1-635 < MUR>
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A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen A;Reference number: A57131; MUID:91210292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A57131
R;Muragaki, Y.; Jac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GPPAHPRPPEEVGPPGAPGLPQYTGEISEM----TKCPCPDIERS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 VAGPPAHP---
                                                                                                                                                                                                                                                                                                                                                                                                                              HCK-VNIWL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAHATPAFTAVLTSPLPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAYHV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSSFDVELHHCKVNIWLMRK
                                                                                                                                                                                                                                                                                                                                                                                        HVKGTNVWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFAYHITVYMKDVKVSLFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----AFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------RPPEEVGPPGAPGLPQYTGEISEMTKCP------CPDIE
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                                                                  conceptual translation
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                                                                                                                               of.
                                                                                                                               the
                                                                                                                             genes encoding
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predicted <NC2>
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                                                                                                                             and C-chains
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A;Experimental source: tissue-type C;Genetics:
A;Note: RIM
C;Function:
A:Note: RIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 29-56, 'P', 58-65, 'K', 67-71, 'P', 73-83, 'K', 85-86, 'D', 88-89, 'N', 91-122 <REI>C;Comment: The first component of complement is a calcium-dependent complex of the th ivation of Clr (enzyme), Cls (proenzyme), and the other eight components of complement C;Comment: The Clq subcomponent is composed of nine subunits, six of which are disulf dimers of the C chain. Equimolar amounts of the A, B, and C chains are found after r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A90304; MUID:80020137 A; Accession: A03207
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                                                                                                                                                                                      A; Description: 1
C; Keywords: GTP
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Rim is a putative Rab3 effector in regulating synaptic-vesicle fusion. A; Reference number: 214897; MUID: 97394473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Wang, Y.; Okamoto, M.;
Nature 388, 593-598, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rab3 effector protein Rim - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
C;Accession: T03301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
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A; Introns: 60/3
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A;Cross-references:
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                                                                                                                                                                                                                                                                                                                                       A;Residues:
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated
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7
PRGPRPP--TVPPPMQELP----DLSHLT-----EEERNIIMAVMDRQKEEEEKE---EA 52
                                       PAHPRPPEEVGPPGAPGLPQYTGEISEMTKCPCPDIERSAFTVKLSGKLPLPFKPIIFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APNSLIRFNAVLTNPQGDYDTSTGKFTCKVPGLYYFVYHAS-HTANLCVLLYRSGV
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                                                                                                                                                                                                                                                                                                                                         1-1553 <WAN>
                                                                                                  Similarity
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                                                                                                                                                                                      Rim protein is binding; zinc
                                                                                   Conservative
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acid s
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                                                                                                                                                                                      proposed as Rab3-dependent regulator of synaptic-vesicl
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2; Mismatches
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brain
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                                                 324 ----EGIADERERKERRETRRLEKGRSQDYSDR-PEK 355
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                                                                                                    216 LSDTATGAGSEVPREKKARLQERSRSQTPLSTAAVSSQDTATPGAPLHRNKGAEPSQQAL 275
                                                                                                                           237 LCCVQ------PRDLVPCV------PVNSAVAS--EGASP------KPWQLPS 269
                                                                                                                                                                                                          102 ERDWRLHQQFESYKEQVRKIGEEARRYQGEHKDDAPTCGICHKTKFADGCGHLCSYCRTK 161
                                                                                                                                                                                                                            141 EVTWVLLKAFSFIREAEHKSSENL-----HPDNV----IKKKNPFSEGKFKLAA----E 186
                                                                                                                                                                                                                                                             53 MLKCVVRDMAKPA---ACKTPRNAES----QPHQPPLNIF----RCVCVPRKPSSEEGGP 101
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Search completed: June 30, 2002, 11:53:51 Job time: 142 sec

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US-09-118-930-294
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APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EEARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 215
TYPE: PRT
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Sequence 6, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN I
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
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Matches 57
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5256642-1
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US-08-973-675-2
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Pred. No. 7.3e-14;
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; ORGANISM: Tamias sibricus
US-09-140-804-6
                                                                            ; MOLECULE TYPE: US-08-463-911-3
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Matches 47; Conservative 15; Mismatches
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Patent No. 5869330
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LENGTH: 236
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Best Local Similarity
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EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                           TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                             NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Scherer, Philipp E. APPLICANT: Lodish, Harvey F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 3.7e-09;
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 Score 167; DB 2;
Pred. No. 1.2e-08;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Scherer, APPLICANT: Lodish,
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                 149 A-----FSFIREAEHKSSENLHPDNV 169
208 LEVGDQVWLQVYGDGDH---NGLYADNV
                                                                   148 GSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 QQSIQEVT 143
                                                                                                                                                                                                                                                                                                                          LENGTH: 247 amin TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Lexington
STATE: Massachu:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                 91 EAMGVFACRVPGNYYSSFDVELH--HCKVNIWLMRKQILANKEEISKQQSIQEVTWVLLK 148
                                                                                                                                      93 GPRGFPGTPGRKGEPGEAAY-----MYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYD 147
                                                                                                                                                                      31 GPPGAPGLPQYTGEISEMTKCPCPDIERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELHHCKVNIWLMRKQILANKEEISK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPPGTPGKP---GPPGWNGFPGLPGPPGPPGMTVNCHSKG--TSAFAVKANELPPAPSQP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2, Application US/08463911
5, 5869330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                             6.1%; Sur
29.7%; Prev
23;
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Harvey F.
A NOVEL SERUM PROTEIN PRODUCED
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                                                                                                                                                                                                                      Score 152.5; DB 2; Pred. No. 5.3e-07;
                                                                                                                                                                                                        Mismatches
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US-08-463-911-7
                                                                                                                                                                                                                      US-09-140-804-3
                                                                             GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                               Sequence 3, Application US/09140804 Patent No. 6197930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 30.7 Matches 43; Conservative
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CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRECTORIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 861-95
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                           105 YSSFDVELHHCKVNIWLMRK 124
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                 99 GRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLY 158
                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 MAGIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGE-TGVPGAEGPRGFPGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 VAGPPAHP------RPPEEVGPPGAPGLPQYTGEISEMTKCP-----CPDIE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                  -----RSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lexington
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RESULT 8
US-09-118-408-3
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-804-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens US-09-140-804-8
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 247
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09140804 Patent No. 6197930
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Best Local S
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Best Local Similarity
Matches 43: Consery
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                                                                                                                                                                             SSFDVELH--HCKVNIWLMRKQILANKEEISKQQSIQEVTWVLLKA-----FSFIREA 156
                                                                                                       EHKSSENLHPDNV 169
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                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 144.5; DB 4
26.4%; Pred. No. 3.3e-06;
tive 25; Mismatches 74
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Sequence 3, Application US/09118408A Patent No. 6265544

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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEG ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 295
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US-09-188-930-295
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                                                                                                                                                        Query Match
Best Local Similarity 31.9
Matches 38; Conservative
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LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 295,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 615050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/118,408A CURRENT FILING DATE: 1998-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 97-30
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                        ENGTH:
112 ESRVPPPADTPLPFDRVLLNEQGHYDATTGKFTCQVPGVYYFAVHATVYRASLQFDLVK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 SSFDVELH--HCKVNIWLMRKQILANKEEISKQQSIQEVTWVLLKA-----FSFIREA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 EHKSSENLHPDNV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 FSYHITVYMKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 RKGEPGEAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56
                                                                                  54 GRDGAPGAPGEKGEGGRPGLPGPRGEPGPRGEAGPVGAIGPAGECSVP--PRSAFSAKRS 111
                                                                                                                           19 GPPAHPRPPEEVGPPGAPGLPQYTGE-----ISEMTKCPCPDIERSAFTVKLS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 MAGIPGHPGHNGTPGRDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPQTPG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 VAGPPAHP------RPPEEVGPPGAPGLPQYTGEISE--MTKCPCPD------
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                                         -GKLPLPF-KPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELHHCKVNIWLMR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DH---NGLYADNV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                        243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09188930A
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                                                                                                                                                              5.0%; Score 124; DB 4; Length 243; 31.9%; Pred. No. 0.00034; tive 12; Mismatches 53; Indels
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US-09-188-930-294
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                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 294
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Best Local (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/056,983 EARLIER FILING DATE: 1997-08-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sheppard, Paul O. APPLICANT: Humes, Jacqueline M.
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 47
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 VSGTPGKHGIPGKKGPKGKKGEPGLPG-----PCSCGSSRAKSAFSVAVTKSYPRERLP 175
                                                                                                                                                              Local Similarity nes 42; Conserv
  91
                                       45 -ISEMTKCPCPDIERSAFTVKLS-GKLPLPF-KPIIFTGVLYNAQRDLKEAMGVFACRVP 101
                                                                                                                        14 HVEVAGPPAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 VAGPPAHPRPPEEVGPPGAPGLPQYTGEISEMTKCPCPDIE-RSAFTVKLSGKLPLPFKP 75
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PTGPAGECSVP--PRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVP 148
                                                                                 HPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDPGPRGEAGPAG 90
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                                                                                                                      -----PRPPEEVGPPGAPGLPQYTGE------ 44
                                                                                                                                                           Score 121.5; DB 4
Pred. No. 0.00059;
5; Mismatches 57
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                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                Indels
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: LOCATION: 1..130
: OTHER INFORMATION: fragment 118..247
US-09-485-316A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-485-316A-13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 634444
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                                                                 SEQ ID NO 13
                                                                                                                        CURRENT APPLICATION NUMBER: US/09/485,316A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: FR 97/10088
PRIOR FILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: FCT IB98/01256
PRIOR FILING DATE: 1998-08-06
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                                                                                                                                                                                                                                                                                       APPLICANT: Bouqueleret, Lydie
APPLICANT: Yen-Potin, Frances
TITLE OF INVENTION: Lipoprotein-regulating medicaments
FILE REFERENCE: GENSET.036APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bougueleret, Lydie APPLICANT: Yen-Potin, Frances TITLE OF INVENTION: Lipportein-regulating FILE REFERENCE: GENSET.036APC CURRENT APPLICATION NUMBER: US/09/485,316A CURRENT FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bihain, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: FR 97/10088
PRIOR FILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: PCT IB98/01256
PRIOR FILING DATE: 1998-08-06
                                                                                     SOFTWARE:
                                                                                                        NUMBER OF SEQ ID NOS: 14
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ORGANISM: Mus musculus
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                                           ENGTH: 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDH----NGLYADNV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELH--HCKVN 118
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                                                                                     Parent.pm
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27.18;
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                                                                     Query Match
Best Local Similarity
Matches 80; Conserv
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Best Local :
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                                                                                                                                                                                                                                                                               TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTARTION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-C
TELECOMMUNICATION INFORMATION:
2090 EVEIQTYREKLTSKEECLSSQKLEIDLLKSSKEELNNSLKATTQILEELKKTKMDNLKYV 2149
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22-OCT-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A NO.
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                  116 KVNIWLMRKQILANKEEISKQQ------SIQEVTWVLLKAFSFIREAEHKSSENLHPD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 IWLMRKQILANKEEISKQQSIQEVTWVLLKA-----FSFIREAEHKSSENLHPDNV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Polonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDH----NGLYADNV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEAMGVFACRVPGNYYSSFDVELH--HCKVN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVS 60
                                                                                                                                                                                                                                            ENGTH:
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: California
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                                                                                                                                                                                                                       amino acid
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                            2482 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                       4.4%; Score 110; DB 1; 1
21.4%; Pred. No. 0.3;
tive 52; Mismatches 129;
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Pred. No. 0.
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                                                                                                          Length 2482;
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                                                                         112;
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168 NVIKKKNPFSEGKFKLAAEIC-----

--ICNEELN:----VNPQDNG----

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TOPOLOGY: line;

MOLECULE TYPE: p:

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: HUMAI
US-08-353-700-1
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US-08-353-700-1
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAS: (215) 563-404
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: YEN, TIMOTHY J.

APPLICANT: RATTNER, JEROME B.

TITLE OF INVENTION: NUCLEIC ACID ENCODING A

TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,

TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
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LENGTH: 3248 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 09-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                           NAME: REED, JANET E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILREPTTKSVPV 2440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SK-----KSKKAVMSGIHPAEDTEGTEFEPEGLPEVVKKGFAD-----IPTGKTSP 2367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLGPVVP-----GPSPIPSVTEKRLSSGQNKASGKRQRSSGIWENGGGPTPATPESF 2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *LVPCVPVNSAVASEGASPKP----WQLPSGVEPVGAKKSRIE-VWE-----PPIRF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIKELKETLEEKTKEADEYLDKYCSLLISHEKLEKAKEMLETQVAHLCSQQSKQDSRGSP 2269
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| NQLKKENERAQKMKLLIKSCKQLEEEKEILQKELSQLQAAQEKQKTGTVMDTKVDELTT 2209
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4.4%;
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  Score 110; DB 1;
Pred. No. 0.45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version
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                Length 3248;
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3156 TILREPTTKSVPV 3168
                                                                             3096 YILRRTTMATRTSPRLAAQKLALSPLSLGKENLAESSKPTAGGSRSQKVKVAQRSPVDSG 3155
                                 387 TVVAE-LTKTVGI 398
                                                                                                                     340 RAVRRSPPSSRLQKGRSTDSL------QHVPEKSTDT----QCQPVKAAGMESVPYK 386
                                                                                                                                                                                                          291 QKIYGNPWMPRQKFAV--GVGSSWRTSA------RVVQKGNVGWEPPHRVPSGAPSS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 KVNIWLMRKQILANKEEISKQQ------SIQEVTWVLLKAFSFIREAEHKSSENLHPD 167
                                                                                                                                                                                                                                                                                            -LVPCVPVNSAVASEGASPKP----WQLPSGVEPVGAKKSRIE-VWE------PPIRF 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVEIQTYREKLTSKEECLSSQKLEIDLLKSSKEELNNSLKATTQILEELKKTKMDNLKYV 2877
                                                                                                                                                               SK-----KSKKAVMSGIHPAEDTEGTEFEPEGLPEVVKKGFAD-----IPTGKTSP 3095
                                                                                                                                                                                                                                                    LLGPVVP-----GPSPIPSVTEKRLSSGQNKASGKRQRSSGIWENGRGPTPATPESF 3049
                                                                                                                                                                                                                                                                                                                                                                              --ENISWTCORSSOQS------IKSLAWRPRRKWFCGTGPGSLCCVQPRD----- 244
                                                                                                                                                                                                                                                                                                                                                                                                                           NQLKKENERAQGKMKLLIKSCKQLEEEKEILQKELSQLQAAQEKQKTGTVMDTKVDELTT 2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVIKKNPFSEGKFKLAAEIC-----ICNEELN-----VNPQDNG------ 202
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Search completed: June 30, 2002, 11:53:23 Job time: 144 sec

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to become greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
    766
698
676.5
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length: 2000000000
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Match
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2494
1 IVVIPVLITAVIEH
                                                                                                                                                                                                                                                                                                                               hits satisfying chosen parameters:
   30.7
28.0
27.8
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26.7
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26.2
25.2
24.1
23.0
22.9
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                                                                                                                                                                                                                                                                                                                     SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT: *

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT: *

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT: *

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT: *

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT: *

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT: *

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT: *

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT: *

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SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
                                                                                                                                                                                         Length
    273
939
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439
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 ABG02620
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ALIGNMENTS

RESULT ABG02620

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess WPI; 31-MAR-2000; 23-AUG-2000; W0200175067-A2 Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder. ABG02620; ABG02620 standard; Protein; N-PSDB; (HYSE-) 30-MAR-2001; 2001WO-US08631. 11-OCT-2001. Homo sapiens. Novel human diagnostic protein #2611. 13-FEB-2002 2001-639362/73. DB; AAS66807. HYSEQ INC. RT, Liu C, 2000US-0540217. 2000US-0649167. (first entry) Tang TY 332 ₿

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CC Specification, but was obtained in electronic format directly from WIPO as term vince in the printed content of the invention.
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food supplement; medical imaging; diagnos
                  Homo sapiens
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52.5%;
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Pred. No. 4.4e-59;
22; Mismatches 73;
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The composition are also used in diagnostics as expressed sequence tags comply to restore normal activity of (II) is useful in gene therapy techniques comparating and in the composition of (II). The composition is useful for generating antibodies against it, detecting or comparating a polyment of (II) and its binding partners are useful in medical comparating of sites expressing (II). (I) and (II) are useful for treating comparating or comparating of sites expressing (II). (I) and (II) are useful for treating comparing of sites expressing (II). (I) and (II) are useful in medical comparating of sites expressing (II). (I) and (II) are useful for treating comparating of sites expressing (II). (I) and (II) are useful in medical comparating of sites expressing (II). (I) and (II) are useful in medical comparating of sites expressing (II). (I) and (II) are useful in the comparating comparating in the properties and products are useful in medical comparating of the product of specific disorders or other treating comparating comparati
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                                                                                       diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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PPHRVPSGAPSSRAVRRSPPSSRLQKGRSTDSLQHVPEKSTDTQCQPVKAA--GMESV--
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                                     phavepvgaqksriedweplprfqkmcgnawmprqkiaagagpswrtsaravqkgnvesq
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                                                                                                                                                                                                                                                                                                                                               psadefadhlgn-sklskcvnfdknpdsfevlsnlnkrkrppwkitemstkrhkrgscns 1585
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44.3%; Pred. No. 5.4e-52;
tive 36; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
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                              Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic (
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2000US-0649167.
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Query Match Best Local

Similarity

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Score Pred.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, undiagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to be a few disorders.
                                                                                                                                                                                          Claim 20;
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forension supplement; medical imaging; diagnostic; genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
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2000US-0649167.
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Best Local :
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
31-MAR-2000;
23-AUG-2000;
                                                                                                           WO200175067-A2
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                                             30-MAR-2001; 2001WO-US08631
                                                                            11-OCT-2001
                                                                                                                                        Homo sapiens
                                                                                                                                                                                    Human;
                                                                                                                                                                                                                      Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAVASEGASPKPW-----QLPSG-----VEPVGAKKSRIEVWEPPIRFQKIYGNPWMPRQK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELNVNPQDNGENISWTCQRSSQQSIKSLAWRPRRKWFCGTGPGSLCCVQPRDLVPCVPVN 252
                                                                                                                                                                       supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAVGVGSSWRTSARVVQKGNVGWEPPHRVPSGAPSSRAVRRSPPSSRLQKGRSTDSLQHV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gakvqlgl----wlqrvqalshgnfhmvgpvgaeksrievwkplpgfqrmygkawmsrqk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKQQSIQEVTWVLLKAFSFIREAEHKSSENLHPDNVIKKKNPFSEGKFKLAAEICICNE 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human diagnostic protein #16674.
                                                                                                                                                                  chromosome mapping; gene mapping; gene therapy;
upplement; medical imaging; diagnostic; genetic (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              939 AA;
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2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                  (first entry)
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AELTKTVGIYLLHCHDLDVRHGVKRDHFGALRFDCPTGFRTYMGPVPLCFGQFFPFGTAV qrvptgappsgtvrrrplssrpqnvrstdslhcvpgkaadtqhqpvkaarreavpckatg

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CC Note: The sequence data for this patent did not appear in the printed CC at fire wino intentionable and products dependent on DNA and CC at the wino intention but was obtained in electronic format directly from WIPO CC at the patent format published patent contents in the printed CC at the patent format directly from WIPO CC at the patent contents are contents.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
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                                                                         717
                                                                                                                                                                                                                                                                                                                                                                                                                128 ANKEEISKQQSIQEVTWVLLKAF--SFIREAEHKSSENLHPDNVIKKKNPFSE---GKF- 181
HRVPSGAPSSRAVRRSPPSSRLQKGRSTDSLQHVPEKSTDTQCQPVKAAGMESVPYKTVV
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DB; AAS80870.
                                                                      gvepagaqksrsevwappprfqkmyrnawmsrqkfatelgsswttsaravrkrnvglept
                                                                                                                   GVEPVGAKKSRIEVWEPPIRFQKIYGNPWMPRQKFAVGVGSSWRTSARVVQKGNVGWEPP
                                                                                                                                                                   ----gfhfyfylissccchprnlvpcvsaapafarrgggvarpivsegaspkpwhlpr
                                                                                                                                                                                                                   FCGTGPG------SLCCVQPRDLVPCVPVNSA------VASEGASPKPWQLPS
                                                                                                                                                                                                                                                                     avgvlegtssmaatrenev----evkvetqdkplrfiw----
                                                                                                                                                                                                                                                                                                                     -----KLAA----EICICNEELNVNPQDNGENISWTCQRSSQQSIKSLAWRPRRKW 228
                                                                                                                                                                                                                                                                                                                                                                     afksndsqqqdvsefthklldwledafqmkaeeetdee-----kpknpmvelfygrfl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.7%; Score 665.5;
44.3%; Pred. No. 1.3
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1; Mismatches
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Best Local
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                                                                                                                                                                                                    the specification. The primer sets can be used in antiseuss the specification. The primers are useful for synthesising polynucleotides, in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of the specification of the sequences defined in the specification of the sequences defined in the specification of the sequences defined in the specification.
                                                                                                                                                                                                                                                                                                                                                                  complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of an oligonucleotide comprising a sequence complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB92981 standard; Protein;
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                                   254 AVASEGASPKPWQLPSGVEPVGAKKSRIEVWEPPIRFQKIYGNPWMPRQKFAVGVGSSWR 313
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133; Conservative
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2000JP-0183767.
2000JP-0241899.
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                                                                         Score 653; DB 22;
Pred. No. 2.3e-49;
5; Mismatches 49;
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                                                                                                           Length 220;
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RESULT
ABG02511
CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II), (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II), (I) and (II) are useful for treating CC disgonstics involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity amino acid sequences of the invention.

CC and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed coat of the printed in the printed coat of the printed 
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to isolated polynucleotide (I) and
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RESULT
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polypeptide (II) sequences. (I) is useful as nyuriussum. Polypeptide (II) sequences. (I) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, us diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to biodiversity
                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                        Claim
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23-AUG-2000;
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DB; AAS80647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  supplement;
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upplement; medical imaging; diagnostic; genetic c
                                                                                                                                                                                                                                                                                                                                       RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                    HYSEQ INC
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to assess
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Claim

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30840; 103pp;

biodiversity

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RESULT

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ABGOUAT

AC ABGO

XX ABGO

XX ABGO

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XX WPI:

DR N-PE

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PT dias

PT Cine

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                                      New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutal responsible for genetic disorders or other traits and to assobiodiversity -
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic (
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                                                                                                                                       WPI;
                                                                                                                                                                                                    (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTVVAELTKTVGIYLLHCHDLDVRHGVKRDHEGALREDCPTGERTYMGP-VPLCEGQEEP 444
                                                                                                                                      2001-639362/73
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2000US-0649167
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                                                                                                                                                                   Liu C,
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602; DB 22;
No 2.1e-44;
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RESULT 10
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CC Note: The sequence data for this patent did not appear in the printed CC at fire veguence data for this patent did not appear in the printed CC at fire. Wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
31-MAR-2000;
                                   30-MAR-2001; 2001WO-US08631.
                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                           Novel human diagnostic protein #16412.
                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                          ABG16421 standard; Protein; 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVPLCFGQFFPFGTAVFT - - QCLYL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVKAAGMESVPYKTVVAELTKTVGIYLLHCHDLDVRHGVKRDHFGALRFDCPTGFRTYMG 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gddfgylaeeiskgqsiqxawe-----lgalcsshsshgkrgqgraw-----
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2000US-0540217
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.0%; Score 573.5; DB 22; 48.3%; Pred. No. 3.1e-42; tive 25; Mismatches 77;
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ches 77;
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RESULT 11 ABG17512 ID ABG175

ABG17512 standard; Protein; 439

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413 plfwpisp

420

437 353 377 293 317 233

LCFGQFFP 444

XXX DXX AX

18-FEB-2002

(first entry)

Human; chromosome mapping; gene mapping; gene therapy; forensic;

Novel human diagnostic protein #17503.

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rtvwkgivgseppyrvptgalpsgaerrgpppsrpqngrsdnslycvpgkstdtqcqpvk 352

RVVQKGNVGWEPPHRVPSGAPSSRAVRRSPPSSRLQKGRSTDSLQHVPEKSTDTQCQPVK 376 slsvsqrpvsasaaagstalqksrievwepvrrfqkiygnswtpwqkfaagvgpswgtsa 292

SEGASPKPWQLPSGVEPVGAKKSRIEVWEPPIRFQKIYGNPWMPRQKFAVGVGSSWRTSA 316

Conservative

10;

Mismatches

61;

Indels

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Gaps

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CC polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The complex com
Query Match
Best Local Similarity
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                                                                                                                                      Sequence
                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 46780; 103pp; English.
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                                                                                                                                      439 AA;
22.9%; Score 570; DB 22; 62.2%; Pred. No. 1.2e-41;
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                           Length 439;
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of mutations
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CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at figure in the printed content in the
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase chain reaction (PCR) primers, o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS81699.
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                                                                                                                                                                                                                                                                                                slsvsqrpvsasaaagstalqksrievwepvrrfqkiygnswtpwqkfaagvgpswgtsa 292
                                                                                                                                                                                                                                                                                                                          SEGASPKPWQLPSGVEPVGAKKSRIEVWEPPIRFQKIYGNPWMPRQKFAVGVGSSWRTSA 316
                                                                                                                                                                                                                       RVVQKGNVGWEPPHRVPSGAPSSRAVRRSPPSSRLQKGRSTDSLQHVPEKSTDTQCQPVK 376
plfwpisp 420
                                                 LCFGQFFP 444
                                                                                                                       AAGMESVPYKTVVAELTKTVGIYLLHCHDLDVRHGVKRDHFGALRFDCPTGFRTYMGPVP 436
                                                                                                                                                                                             rtvwkgivgseppyrvptgalpsgaerrgpppsrpqngrsdnslycvpgkstdtqcqpvk
                                                                                             aagreglpckatgvelsktigthllhqcdldvrsgvkgdhfgaltfdcpagfrtcmgpvt 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 570; DB Pred. No. 1.2e
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1.2e-41;
nes 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 439;
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172.KKNPFSEGKFKLAAEICICNEELNV-NPQDNGENISWTCQRSSQQSIKSLAWRPR---RK

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RESULT 1
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CC Note: The sequence data for this patent did not appear in the printed content of the printed of the 
                                                                                             Matches
                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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23-AUG-2000;
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                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
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                            CKVNIW---LMRKQILANKEEISKQQSIQEVTWVLLKAFSFIREAEHKSSENLHPDNVIK 171
cprdlwnfelerddlgylveeiskqqsiqe------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                           261
                                                                                           Conservative
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2000US-0649167
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                                                                                                                21.7%;
48.7%;
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                                                                                 Score 540.5; DB zz;
Pred. No. 2.4e-39;
""smatches 68;
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d to assess
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                                                                                        Gaps
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RESULT
ABG02632
          CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or creating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequences of the invention.

CC and to produce other types of data and products dependent on DNA and constitutions in the printed constitution of the invention.

CC and to produce other types of data and products dependent on DNA and constitutions in the printed constitution, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                         Claim 20;
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            supplement;
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                         ID No 32991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mapping; gene mapping; gene therapy; forensic
medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                     103pp;
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                                                                                                                                                                                                                                                                                                                                                                     English
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Matches
       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chrome and gene mapping, and in recombinant production of (II). The
                                                                                            biodiversity
                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG17044;
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                                                                     Claim
                                                                                                                                                      N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKNPFSEGKFKLAAEICICNEELNV-NPQDNGENISWTCQRSSQQSIKSLAWRPR---RK 227
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                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                      2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                     ID No 47403;
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48.7%;
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                                                                   103pp; English.
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Pred. No. 2.4
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also · used

expressed sequence tags

chromosome

Claim 20;

SEQ ID No 57991; 103pp;

English

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В
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CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO at first products.
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Best Local Similarity
Matches 104; Conserv
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                   WPI; 2001-639362/73.
N-PSDB; AAS91819.
                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                           Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #27623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG27632 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG27632;
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                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 DLDVRHGVKRDHFGALRFDCPTGFRTYMGPVPLCFGQF 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 EPPIREQKIYGNPWMPRQKFAVGVGSSWRTSARVVQKGNVGWEPPHRVPSGAPSSRAVRR 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 dldvrhgvkgdhigalrfdcvagfltsmgpvspcfgey 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 gppfsrpqngrstgslhhvhgkaadaqdqpvkaagreaisckskgaelpktrgthllhqr 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 eypaifqkmygnawmprkkfaagvgpswrtsaramqtgnvglepthripsgalpcgavrr 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPPSSRLQKGRSTDSLQHVPEKSTDTQCQPVKAAGMESVPYKTVVAELTKTVGIYLLHCH 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping; gene mapping; gene therapy; forensinupplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                    RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         766 AA;
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                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.2%; Score 528; DB 22; Length 766; 65.8%; Pred. No. 1.4e-37; tive 11; Mismatches 43; Indels
                                                                                                                                                                                                                                                                       YT;
                                                                 mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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cc and gene mapping, and in recombinant production of (II). The coplynucleotides are also used in diagnostics as expressed sequence tags cfor identifying expressed genes. (I) is useful in gene therapy techniques ct restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or cquantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cd disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cd diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cd amino acid sequences. Abg00010-Abg30377 represent novel human diagnostic amino acid sequence after this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
Query Match
Best Local Similarity
Matches 121; Conserv
                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                            636 AA;
  Conservative
                             21.0%;
24;
                          Score 523; DB 22;
Pred. No. 2.9e-37;
  Mismatches
                                               Length 636;
  Indels
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1spf 310
                                                                                      VPYKTVVAELTKTVGIYLLHCHDLDVRHGVKRDHFGALRF-DCPTGFRTYMGPVPLCFGQ
                                                                                                                                                                                                                          LPSGVEPVGAKKSRIEVWEPPIRFQKIYGNPWMPRQKFAVGVG----SSWRTSARVVQKG
                                                                                                                                                                                                                                                                                             RPR----RKWFCGTGPGSLCCVQPRDLV-------PCV---PVNSAVASEGASPKPWQ 266
                                                                                                                                                                        NVGWEPPHRVPSGAPSSRAVRRSPPSSRLQKGRSTDSLQHVPEKSTDTQCQPVKAAGMES 382
                                                                   vpcrapsreipkaleahplheccldvrhgvkgdhfgalrfndcpagfqtymgpvaplfwl
                                                                                                                                      nvglepphrvsagalpsgvvtrgplssrpqngrsidslycvpgnatvtkcqlvkaa-ega
                                                                                                                                                                                                        lshsvkpvgvertrveaweppprfqrmygncwm-----vevgyraepswrtstravqrg
                                                                                                                                                          441
                                                                                                                                                                                                                                           322
                                                                                                                                                                                                          187
                                                                                                                                        246
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Search completed: Job time: 236 sec June 30, 2002, 11:53:00